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OY		2398	ACGAGAGAGAGAGAGAGAGAGCTCGGGCTCCTCTCGAAAAATTTAAATTTTTAAA	2457
Dd		444	ACGAGAGAGAGAGAGAGAGCTCGGGCTCCTCTCGAAAAATTTAAATTTTTAAA	503
OY		2458	TAAATTTTAAATAATTAATTAATCACTAATACACTATTAAAGAAATTAAGAAGTC	2517
Dd		504	TAAATTTTAAATAATTAATTAATCACTAATACACTATTAAAGAAATTAAGAAGTC	563
OY		2518	TCAGTTTGACGTATTGTGC AAAATTAATATACATTTCTTTTATACAGGAATATTCG	2577
Dd		564	TCAGTTTGACGTATTGTGC AAAATTAATATACATTTCTTTTATACAGGAATATTCG	623
OY		2578	GCAATTATAGATCTCGAATTTTGACCATTATAGAACGCCCAACACAGGCTTTGAGG	2637
Dd		624	GCAATTATAGATCTCGAATTTTGACCATTATAGAACGCCCAACACAGGCTTTGAGG	683
OY		2638	TCTTGSCAATCTTGCGTAGATTGGCTGTCCCAATGTTTACATTAATTAATCTTGCAAA	2697
Dd		684	TCTTGSCAATCTTGCGTAGATTGGCTGTCCCAATGTTTACATTAATTAATCTTGCAAA	743
OY		2698	ATGCTTCTGTGCACTTGGAATGTGAATAGCTGTCCAGTTTATTTTATATGTGTATTC	2755
Dd		744	ATGCTTCTGTGCACTTGGAATGTGAATAGCTGTCCAGTTTATTTTATATGTGTATTC	803
OY		2758	CTTGAGATGTACA AAAAATTCAGAAAATGATCTGTAGATATTCGTATTATTTTGTCA	2817
Dd		804	CTTGAGATGTACA AAAAATTCAGAAAATGATCTGTAGATATTCGTATTATTTTGTCA	863
OY		2818	TCTTTAGAAAGTTTACAGGAATGTGTTTAAACAAGAGAGAACTTCTTAGAAGATATA	2877
Dd		864	TCTTTAGAAAGTTTACAGGAATGTGTTTAAACAAGAGAGAACTTCTTAGAAGATATA	923
OY		2878	CATPAGAAAAGTTTATTTTAAATTAAGATGTGAAGCTGTGCTTCTTGCTGCTGAG	2937
Dd		924	CATPAGAAAAGTTTATTTTAAATTAAGATGTGAAGCTGTGCTTCTTGCTGCTGAG	983
OY		2938	CTATCGCCCAAGTATAGCAATGGAAGCACTTTTATAGTACAGAAA-----AC	2987
Dd		984	CTATCGCCCAAGTATAGCAATGGAAGCACTTTTATAGTACAGAAA-----AC	1043
OY		2988	AAC	3047
Dd		1044	AAC	1103
OY		3048	CTTTTCTTAACTCCCTCTTGACGCTGTGTGTGAGACACCTGTTTATTTCTCTAATAT	3107
Dd		1104	CTTTTCTTAACTCCCTCTTGACGCTGTGTGTGAGACACCTGTTTATTTCTCTAATAT	1163
OY		3108	ATGTCAGTTTATTTCTTTTATATGACCTATAAAAAATGTATATCACAGAGTCCAANT-T	3166
Dd		1164	ATGTCAGTTTATTTCTTTTATATGACCTATAAAAAATGTATATCACAGAGTCCAANT-T	1223
OY		3167	CTTGAAATGCCCAAAGGCTTTT 3188	
Dd		1224	CTTGAAATGCCCAAAGGCTTTT 1245	
 RESULT 2 US-09-566-921-70 Sequence 70, Application US/09566921 Patent No. 6682888 GENERAL INFORMATION: APPLICANT: Loring, Jeanne F. APPLICANT: Tingler, Debora W. APPLICANT: Edwards, Carl A. TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE FILE REFERENCE: PA-0024 US CURRENT APPLICATION NUMBER: US/09/566,921 FILING DATE: 2000-05-05 NUMBER OF SEQ ID NOS: 138 SOFTWARE: PERL Program SEQ ID NO 70 LENGTH: 1876				

[illegible]

1115 Page Blank (uspio)

QY 3050 TTTTCTACTCCCTTGAGCTCTCTGTGAGCAGCTTATTCTTAAATAT 3109
 DB 1420 TTTTCTACTCCCTTGAGCTCTCTGTGAGCAGCTTATTCTTAAATAT 1479
 QY 3110 GTGAGTTATCTCTTAAATGAGCTGTAATAATGATCAAGAGTCCAAAT-TCT 3168
 DB 1480 GTGAGTTATCTCTTAAATGAGCTGTAATAATGATCAAGAGTCCAAATATCT 1539
 QY 3169 TGAATGCAAAAGGCTTTT 3188
 DB 1540 TGAATGCAAAAGGCTTTT 1559

RESULT 3
 US-09-513-999C-10663
 ; Sequence 10663, Application US/09513999C
 ; Patent No. 6783961
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Ducielt, A. Y.
 ; APPLICANT: Giordano, J. Y.
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 ; Patent No. 6783961
 ; FILE REFERENCE: 59, US2, REG
 ; CURRENT APPLICATION NUMBER: US/09/513, 999C
 ; CURRENT FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/122,487
 ; NUMBER OF SEQ ID NOS: 36681
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 10663
 ; LENGTH: 524
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 465
 ; OTHER INFORMATION: r=a or g
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 471
 ; OTHER INFORMATION: n=a, g, c or t
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 475
 ; OTHER INFORMATION: r=a or g
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 488
 ; OTHER INFORMATION: k=g or t
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 491
 ; OTHER INFORMATION: m=a or c
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 497
 ; OTHER INFORMATION: y=c or t
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 510
 ; OTHER INFORMATION: k=g or t
 ; OTHER INFORMATION: k=g or t
 ; US-09-513-999C-10663

Query Match 15.9%; Score 507; DB 3; Length 524;
 Best Local Similarity 98.5%; Pred. No. 6,5e-90;
 Matches 516; Conservative 5; Mismatches 1; Indels 2; Gaps 1;

QY 2618 CAACACAGGTTTGTGAGTGTGAGCTTCTTGGCTATTTGGCTGTCCAAATTTTA 2677
 DB 61 CAACACAGGTTTGTGAGTGTGAGCTTCTTGGCTATTTGGCTGTCCAAATTTTA 120
 QY 2678 CATTATTTATCTTGCAAAATGTTCTGTGACCTTGATGTAATGCTGTCCAGTTT 2737
 DB 121 CATTATTTATCTTGCAAAATGTTCTGTGACCTTGATGTAATGCTGTCCAGTTT 180
 QY 2738 ATTATTTTATGTTGTTATCTTGATGTAATGTAATGTAATGATCTGTGAT 2797
 DB 181 ATTATTTTATGTTGTTATCTTGATGTAATGTAATGTAATGATCTGTGAT 240
 QY 2798 ATTCTGTTTATTTGTCATCTTTAGAGTTATCAGAAATGTTTAAACAGAGAG 2857
 DB 241 ATTCTGTTTATTTGTCATCTTTAGAGTTATCAGAAATGTTTAAACAGAGAG 300
 QY 2858 AACCTTTCTAGAGATGATACATGAAATGTAATTTTAAATGAGTTGTAACCTTG 2917
 DB 301 AACCTTTCTAGAGATGATACATGAAATGTAATTTTAAATGAGTTGTAACCTTG 360
 QY 2918 TGTTTCTTGTGTCGCAAGCTATCTGCAAGTTAATGCAAAATGACATTTTATG 2977
 DB 361 TGTTTCTTGTGTCGCAAGCTATCTGCAAGTTAATGCAAAATGACATTTTATG 420
 QY 2978 TGAAGAAAC 3035
 DB 421 TGAAGAAAC 480
 QY 3035 AAAATGCTTGAAGCTTTTCTTAACCTTCCCTTGACATCTGTGTG 3079
 DB 481 AAAATGCTTGAAGCTTTTCTTAACCTTCCCTTGACATCTGTGTG 524

RESULT 4
 US-09-702-705-475/c
 ; Sequence 475, Application US/09702705
 ; Patent No. 6504010
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tonglong
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Lodges, Michael A.
 ; APPLICANT: Fanger, Gary
 ; APPLICANT: Vedvik, Tom
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Retter, Marc
 ; APPLICANT: Mannion, Jane
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.478C14
 ; CURRENT APPLICATION NUMBER: US/09/702,705
 ; CURRENT FILING DATE: 2000-10-30
 ; NUMBER OF SEQ ID NOS: 1833
 ; SOFTWARE: Fasteq for Windows Version 3.0
 ; SEQ ID NO 475
 ; LENGTH: 417
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(417)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-702-705-475

Query Match 13.0%; Score 413.4; DB 3; Length 417;
 Best Local Similarity 99.3%; Pred. No. 1.3e-71;
 Matches 414; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 357 TAAAGAAATCTCACTGACCTATTTGTCACAAATTAATCCATTTCTTTTAAATAC 298
Qy 2566 GGTGAATATTGGCAATTAATGATCTGATTTGAACCACTAATGAAGGCAACACA 2625
Db 297 GGTGAATATTGGCAATTAATGATCTGATTTGAACCACTAATGAAGGCAACACA 238
Qy 2626 GGTGTTTGAAGTGTGGCAATTTCTGATTTGGCTGTTCCCAATGTTAATATT 2685
Db 237 GGTGTTTGAAGTGTGGCAATTTCTGATTTGGCTGTTCCCAATGTTAATATT 178
Qy 2686 AATCTTGCAAAAATGGTCTGTCGACCTTGAGATGCGACGTTTATTTT 2745
Db 177 AATCTTGCAAAAATGGTCTGTCGACCTTGAGATGCGACGTTTATTTT 118
Qy 2746 TATGTTGTTATCCTTGAGATGTCACAAAATTCAGAAAATGATCTGTAGATCTGTT 2805
Db 117 TATGTTGTTATCCTTGAGATGTCACAAAATTCAGAAAATGATCTGTAGATCTGTT 58
Qy 2806 TTATTTTGGTCATCTTTAGAAAGTTATCAGGAATGTGTTTAAACAAGAGAACTT 2862
Db 57 TTATTTTGGTCATCTTTAGAAAGTTATCAGGAATGTGTTTAAACAAGAGAACTT 1
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RESULT 5

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US-09-736-457-475/C
; Sequence 475, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Patrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Lijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO: 475
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(417)
; OTHER INFORMATION: n = A,T,C or G
US-09-736-457-475
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Query Match 13.0%; Score 413.4; DB 3; Length 417;
Best Local Similarity 99.3%; Pred. No. 1.3e-71;
Matches 414; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2446 TAAAGAAATCTCACTGACCTATTTGTCACAAATTAATCCATTTCTTTTAAATAC 2505
Db 417 TAAAGAAATCTCACTGACCTATTTGTCACAAATTAATCCATTTCTTTTAAATAC 358
Qy 2506 TAAAGAAATCTCACTGACCTATTTGTCACAAATTAATCCATTTCTTTTAAATAC 2565
Db 357 TAAAGAAATCTCACTGACCTATTTGTCACAAATTAATCCATTTCTTTTAAATAC 298
Qy 2566 GGTGAATATTGGCAATTAATGATCTGATTTGAACCACTAATGAAGGCAACACA 2625
Db 297 GGTGAATATTGGCAATTAATGATCTGATTTGAACCACTAATGAAGGCAACACA 238
Qy 2626 GGTGTTTGAAGTGTGGCAATTTCTGATTTGGCTGTTCCCAATGTTAATATT 2685
Db 57 GGTGTTTGAAGTGTGGCAATTTCTGATTTGGCTGTTCCCAATGTTAATATT 2685
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Db 237 GGTGTTTGAAGTGTGGCAATTTCTGATTTGGCTGTTCCCAATGTTAATATT 178
Qy 2686 AATCTTGCAAAAATGGTCTGTCGACCTTGAGATGCGACGTTTATTTT 2745
Db 177 AATCTTGCAAAAATGGTCTGTCGACCTTGAGATGCGACGTTTATTTT 118
Qy 2746 TATGTTGTTATCCTTGAGATGTCACAAAATTCAGAAAATGATCTGTAGATCTGTT 2805
Db 117 TATGTTGTTATCCTTGAGATGTCACAAAATTCAGAAAATGATCTGTAGATCTGTT 58
Qy 2806 TTATTTTGGTCATCTTTAGAAAGTTATCAGGAATGTGTTTAAACAAGAGAACTT 2862
Db 57 TTATTTTGGTCATCTTTAGAAAGTTATCAGGAATGTGTTTAAACAAGAGAACTT 1
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RESULT 6

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US-09-614-124B-475/C
; Sequence 475, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Patrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO: 475
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(417)
; OTHER INFORMATION: n = A,T,C or G
US-09-614-124B-475
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Query Match 13.0%; Score 413.4; DB 3; Length 417;
Best Local Similarity 99.3%; Pred. No. 1.3e-71;
Matches 414; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2446 TAAAGAAATCTCACTGACCTATTTGTCACAAATTAATCCATTTCTTTTAAATAC 2505
Db 417 TAAAGAAATCTCACTGACCTATTTGTCACAAATTAATCCATTTCTTTTAAATAC 358
Qy 2506 TAAAGAAATCTCACTGACCTATTTGTCACAAATTAATCCATTTCTTTTAAATAC 2565
Db 357 TAAAGAAATCTCACTGACCTATTTGTCACAAATTAATCCATTTCTTTTAAATAC 298
Qy 2566 GGTGAATATTGGCAATTAATGATCTGATTTGAACCACTAATGAAGGCAACACA 2625
Db 297 GGTGAATATTGGCAATTAATGATCTGATTTGAACCACTAATGAAGGCAACACA 238
Qy 2626 GGTGTTTGAAGTGTGGCAATTTCTGATTTGGCTGTTCCCAATGTTAATATT 2685
Db 237 GGTGTTTGAAGTGTGGCAATTTCTGATTTGGCTGTTCCCAATGTTAATATT 178
Qy 2686 AATCTTGCAAAAATGGTCTGTCGACCTTGAGATGCGACGTTTATTTT 2745
Db 177 AATCTTGCAAAAATGGTCTGTCGACCTTGAGATGCGACGTTTATTTT 118
Qy 2746 TATGTTGTTATCCTTGAGATGTCACAAAATTCAGAAAATGATCTGTAGATCTGTT 2805
Db 117 TATGTTGTTATCCTTGAGATGTCACAAAATTCAGAAAATGATCTGTAGATCTGTT 58
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? APPLICANT: Fan, Liqun
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
? TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
? FILE REFERENCE: 210121.478c11
? CURRENT APPLICATION NUMBER: US/09/658, 824
? CURRENT FILING DATE: 2000-09-08
? NUMBER OF SEQ ID NOS: 1788
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 475
? LENGTH: 417
? TYPE: DNA
? ORGANISM: Homo sapien
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1)..(417)
? OTHER INFORMATION: n = A,T,C or G
? US-09-658-824-475

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Best Local	Similarity	99.3%	Pred. No. 1.3e-71		
Matches	444	Conservative	0	Mismatches	3
				Indels	0
				Gaps	0
Qy	2446	TTAAAAATTAATPAAATTTTAAAAATTAATPAAAAATTCCTATATACATATPAAAGAA	2505		
Db	417	TTAAAAATTAATPAAATTTTAAAAATTAATPAAAAATTCCTATATACATATPAAAGAA	358		
Qy	2506	TTAAAAAGATCTGCAGTCGACGCTTTTGCCAAAATTAATATCCATCTCTTTTATATAC	2565		
Db	357	TTAAAAAGAGCTCAGTGGACGATTTTGCCAAAATTAATATCCATCTCTTTTATATAC	298		
Qy	2566	GGTGAAATTTGCGCAATTAATAGTTCGATTTTGAAACAATTAAAGAGGGGGAACA	2625		
Db	297	GGTGAAATTTGCGCAATTAATAGTTCGATTTTGAAACAATTAAAGAGGGGGAACA	238		
Qy	2626	GGGTGTTTGAGGTGTCGCAATCTTCGCTGATTTGGCTGTGTCGCAATGTTAAATATTT	2685		
Db	237	GGGTGTTTGAGGTGTCGCAATCTTCGCTGATTTGGCTGTGTCGCAATGTTAAATATTT	178		
Qy	2686	AATCTTGCAAAAATGGTTCGTGCGCACTTGAGATGCGAAATGCGTTCGAGTTTATTTTTT	2745		
Db	177	AATCTTGCAAAAATGGTTCGTGCGCACTTGAGATGCGAAATGCGTTCGAGTTTATTTTTT	118		
Qy	2746	TATGTGTATCTCTTGAGATGTAACAAAAATTCAGAAATGATCTCTGTAGATATCTGTT	2805		
Db	117	TATGTGTATCTCTTGAGATGTAACAAAAATTCAGAAATGATCTCTGTAGATATCTGTT	58		
Qy	2806	TTATTTTGTGATCTTTAGAGATTTATCGAGATGTGTTTAAACAGAGAGAACTT	2862		
Db	57	TTATTTTGTGATCTTTAGAGATTTATCGAGATGTGTTTAAACAGAGAGAACTT	1		

Oy	2506	TAAAGAAAGCTCAGTTGACAGCTATTTTGCATAAATTAATATCATTTCTTTTATATAC	2565
Oy	357	TAAAGAAAGCTCAGTTGACAGCTATTTTGCATAAATTAATATCATTTCTTTTATATAC	298
Oy	2566	GGGAATATTCGCAATTATATAGATCTGATTTTGAACCACTATATAGACGGCAACCA	2625
Oy	297	GGGAATATTCGCAATTATATAGATCTGATTTTGAACCACTATATAGACGGCAACCA	238
Oy	2626	GGGTTTGAAGTGTGGCAATCTTCGCTGATTTTGGCTGTCCCAATGTTTACATATTT	2685
Oy	237	GGGTTTGAAGTGTGGCAATCTTCGCTGATTTTGGCTGTCCCAATGTTTACATATTT	178
Oy	2686	AATCTGGCAAAAATGGTCTGTGACATCTGGATGTGAATAGCTGTCAAGTTTATTTT	2745
Oy	177	AATCTGGCAAAAATGGTCTGTGACATCTGGATGTGAATAGCTGTCAAGTTTATTTT	118
Oy	2746	TATGTGTATCTCTGGATGTACAAAAATTCGAAATGATCTGTGATATTTCTGT	2805
Oy	117	TATGTGTATCTCTGGATGTACAAAAATTCGAAATGATCTGTGATATTTCTGT	58
Oy	2806	TATTTTGGTATCTTTAGAGATATACAGAAATGTGTTTAAACAAGAGAACTT	2862
Oy	57	TATTTTGGTATCTTTAGAGATATACAGAAATGTGTTTAAACAAGAGAACTT	1

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1 RESULT 10
2 US-10-017-754-475/c
3 ; Sequence 475, Application US/10017754
4 ; Patent No. 6858204
5 ;
6 ; GENERAL INFORMATION:
7 ;
8 ; APPLICANT: Henderson, Robert A.
9 ; APPLICANT: Wang, Tongtong
10 ; APPLICANT: Matanabe, Yoshihiro
11 ; APPLICANT: Johnson, Jeffrey C.
12 ; APPLICANT: Retter, Marc W.
13 ; APPLICANT: Marnetakis, Margarita
14 ; APPLICANT: Carter, Darriek
15 ; APPLICANT: Fanger, Gary R.
16 ; APPLICANT: Vedvick, Thomas S.
17 ; APPLICANT: Bangur, Chaitanya S.
18 ; APPLICANT: McNabb, Andria
19 ;
20 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
21 ; OF INFECTION: AND DIAGNOSIS OF LUNG CANCER
22 ;
23 ; FILE REFERENCE: 210121.478C18
24 ;
25 ; CURRENT APPLICATION NUMBER: US/10/017, 754
26 ;
27 ; CURRENT FILING DATE: 2001-10-29
28 ;
29 ; NUMBER OF SEQ ID NOS: 2004
30 ;

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```

APPLICANT: Lodes, Michael A.
APPLICANT: Fager, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darlick
APPLICANT: Retter, Marc
APPLICANT: Hamilton, Jane
APPLICANT: Fan, Liguu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: IMAGING OF LUNG CANCER
FILE REFERENCE: 21012179C10
CURRENT APPLICATION NUMBER: 09/551,563
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 1679
SOFTWARE: fastseq for windows Version 3.0
SEQ ID NO: 475
LENGTH: 417
TYPE: DNA
ORIGIN: Homo sapien
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(417)
OTHER INFORMATION: n = A, T, C or G

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 21:29:14 ; Search time 5563.2 Seconds
(Without alignments)
11280.402 Million cell updates/sec

Title: US-10-071-645-1

Sequence: 1 ggcacgagcgagcgccgctg.....aaaaaaaaaaaaaaaaaaaa 1104

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Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 2842125653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_cm:*
5: gb_cv:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_hlg:*
15: gb_pl:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1104	100.0	1104	6	AX451459 Sequence
2	803.8	72.8	1876	6	AR454597 Sequence
3	790	71.6	1581	6	BD276315 MOLECULES
4	790	71.6	1581	6	AX049462 Sequence
5	632.6	57.3	1321	6	CQ776764 Sequence
6	607.2	55.0	3189	6	AX451461 Sequence
7	607.2	55.0	126141	14	AL356300 Homo sapi
8	607.2	55.0	195076	8	AL391357 Homo sapi
9	605	54.8	1377	8	BC020630 Homo sapi
10	600.6	54.4	163801	14	AC026224 Homo sapi
11	441	39.9	860	8	AY204501 Homo sapi
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13	427.2	38.7	524	6	AX894800 Sequence
14	405.4	36.7	417	6	BD139338 Extended
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16	295.8	26.8	360	6	CQ699651 Sequence
17	282.2	25.6	411	6	AX330168 Sequence
18	282.2	25.6	411	6	AX332831 Sequence

19	282.2	25.6	411	6	AX334667 Sequence
20	282.2	25.6	411	6	AX335116 Sequence
21	279.4	25.3	409	9	AF271156 Rattus no
22	273.4	24.8	1592	9	AY523601 Mus muscu
23	270	24.5	417	6	AR272746 Sequence
24	270	24.5	417	6	AR272737 Sequence
25	270	24.5	417	6	AR406602 Sequence
26	270	24.5	417	6	AR404042 Sequence
27	270	24.5	417	6	AR472610 Sequence
28	270	24.5	417	6	AR543263 Sequence
29	270	24.5	417	6	AR638421 Sequence
30	270	24.5	417	6	AR628848 Sequence
31	270	24.5	417	6	AX367555 Sequence
32	231.6	21.0	259224	14	AC109006 Rattus no
33	226.8	20.5	170878	14	AC107845 Mus muscu
34	226.8	20.5	248479	9	AL807249 Mouse DNA
35	225.6	20.4	892	10	G28976 human STS S
36	224.4	20.3	237	8	CQ727202 Sequence
37	202	18.3	616	8	HSR224422 Sequence
38	185	14.9	336	6	AR563282 Sequence
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40	155.8	14.1	183	6	BD030206 Sequence
41	155.8	14.1	183	6	AX894673 Sequence
42	133.2	12.1	695	5	CR407503 Gallus ga
43	133.2	11.2	308	6	CQ427555 Sequence
44	133.2	11.2	333	6	CQ418653 Sequence
45	120.4	10.9	347	9	AF041854 Rattus no

ALIGNMENTS

RESULT 1
AX451459
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITRE
JOURNAL
GENSET (FR)

AX451459
Sequence 1 from Patent WO212279.
AX451459
AX451459.1 GI:21698460
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

1
Bihain, B., Bour, B. and Bougueleret, L.
Schizophrenia related gene and protein
Patent: WO 0212279-A 1 14-FEB-2002;
GENSET (FR)

FEATURES
source
1..1104
/organism="Homo sapiens".
/mol_type="unassigned DNA".
/db_xref="taxon:9606"
87..344
/note="unassigned protein product"

CDS
1..1104
/codon_start=1
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/db_xref="GI:21698461"
/translation="MWEVLPYDEKLSPYGDGDVQIFSCRLQPTNNFGAGGNKRP
PRLQIQRSKRVVIEDRIDVLTAKMTDKAPLVNSPKTMS"

ORIGIN
Query Match 100.0%; Score 1104; DB 6; Length 1104;
Best Local Similarity 100.0%; Pred. No. 2.8e-164;
Matches 1104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACGAGCGAGCGCCGCTGACCTGTCGCGCGGCGGAGACGCGGCGGAGAGCGCG 60
DB 1 GGCACGAGCGAGCGCCGCTGACCTGTCGCGCGGCGGAGACGCGGCGGAGAGCGCG 60
QY 61 CCACGCGGAGCGCGCGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 120

61 CCGCGGCGGAGCCCGCGGAGCGACCATGTGGAGTGTGCTTACGGCGACGAGAAC 120
QY 121 TGAAGCCCTTACGGCGAGCGGCGGCGAGCTGGGCGAGATCTTCTCGCGCGCTGACGAGCA 180
Db 121 TGAAGCCCTTACGGCGAGCGGCGGCGAGCTGGGCGAGATCTTCTCGCGCGCTGACGAGCA 180
QY 181 CCAACAACTTTTGGCGCGCGGCGAGCAAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
Db 181 CCAACAACTTTTGGCGCGCGGCGAGCAAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
QY 241 GGAGCAACCGGCGGTTGTTAATGAAAGATGATGATGATGATGATGATGATGATGATGATG 300
Db 241 GGAGCAACCGGCGGTTGTTAATGAAAGATGATGATGATGATGATGATGATGATGATGATG 300
QY 301 ACAAGGCACTCTGAGTGTCTAACTCCCAAGACAAATGATGATGATGATGATGATGATGATG 360
Db 301 ACAAGGCACTCTGAGTGTCTAACTCCCAAGACAAATGATGATGATGATGATGATGATGATG 360
QY 361 GCGGCTAACGTTATGTGGCAAAAGATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 GCGGCTAACGTTATGTGGCAAAAGATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 GCTTGTACCCACGATGAAATCAACAACTGTATGTGTATGTGTATGTGTATGTGTATGTGTAT 480
Db 421 GCTTGTACCCACGATGAAATCAACAACTGTATGTGTATGTGTATGTGTATGTGTATGTGTAT 480
QY 481 CGAG 540
Db 481 CGAG 540
QY 541 AAATTTAAATTAATTAATTCCTATATCCATATAGATTAATTAATTAATTAATTAATTAATTA 600
Db 541 AAATTTAAATTAATTAATTCCTATATCCATATAGATTAATTAATTAATTAATTAATTAATTA 600
QY 601 TTGGCAAAATTAATTCATTTCTTTTAAATCGGGAATATGCAATTAATTAATTAATTAATTA 660
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Db 661 TTGACCACTTAATTAATTAATTCATTTCTTTTAAATCGGGAATATGCAATTAATTAATTAAT 720
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Db 721 TGGCTGTATCCCAATGTGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 780
QY 781 TGAATGCTGTCCAGTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 840
Db 781 TGAATGCTGTCCAGTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 840
QY 841 GAAATGATCTGTGATATCTGTGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTAT 900
Db 841 GAAATGATCTGTGATATCTGTGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTAT 900
QY 901 GTGTTTAAACAG 960
Db 901 GTGTTTAAACAG 960
QY 961 AAATGAGTGAAG 1020
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QY 1021 AATGAGCACTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 1080
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QY 1081 CACGAG 1104
Db 1081 CACGAG 1104

RESULT 2
AK454597

LOCUS AR454597 1876 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 70 from patent US 6682888.
ACCESSION AR454597
VERSION AR454597.1 GI:42688066
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1876)
AUTHORS Loring J.F., Tingley D.W. and Edwards C.M.
TITLE Gene expressed in Alzheimer's disease
JOURNAL Patent: US 6682888-A 70 27-JAN-2004;
Incyte Corporation; Palo Alto, CA
FEATURES
source location/Qualifiers
1..1876
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 72.8%; Score 803.8; DB 6; Length 1876;
Best Local Similarity 87.9%; Pred. No. 6.3e-117;
Matches 991; Conservative 0; Mismatches 103; Indels 34; Gaps 11;
QY 10 CAGCGCGCTGACCTGTCTCGCGCGGCGGAGACGCGGCGGAGAGAGCGCGCGCGG 69
Db 279 CAGCGCGCTGACCTGTCTCGCGCGGCGGAGAGCGGCGGAGAGAGCGCGCGG 338
QY 70 AGCCCCGAGCGGAGCCATGTGGAGAGTGTGCTTACGGCGAGAGAGAGAGAGAGAGAG 129
Db 339 AG-CGCCGAGCGGAGCCATGTGGAGAGTGTGCTTACGGCGAGAGAGAGAGAGAGAGAG 397
QY 130 ACAGGCGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 189
Db 398 ACAGGCGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 457
QY 190 TCTTCGCGCGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 249
Db 458 TCTTCGCGCGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 517
QY 250 GGGTGTATTAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 309
Db 518 GGGTGTATTAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 577
QY 310 CT-CTGAGTCTAACT-CCCAAGACCAATGATGATGATGATGATGATGATGATGATGATGATG 367
Db 578 CTCTGAGTCTAACTCCCAAGACCAATGATGATGATGATGATGATGATGATGATGATGATG 637
QY 368 ACAGTAAATGGCAAAAG 426
Db 638 ACAGTAAATGGCAAAAG 697
QY 427 ACCCAAGATGAATCAACCAACCTGTATCTGTAT-ATGCCGAGAGAGAGAGAGAGAGAGAG 485
Db 698 ACCCAAGATGAATCAACCAACCTGTATCTGTATCAAGCCGAGAGAGAGAGAGAGAGAG 757
QY 486 GAGGAG 545
Db 758 GAGGAG 817
QY 546 TAAATTAAT-----AAATCCCAATATCC-----CAATTAAGATTAAGA 586
Db 818 AAATTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 877
QY 587 GTCTCACT---GCAATATGGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 640
Db 878 GTCTCACTGTGCAAGCATTTGTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 937
QY 641 --TGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 696
Db 938 TGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 997
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Db 998 AGGTGGGCAATCTTCCTGCTGATTTGGCTGTCCTCCAAATGTTTAACTTATCTTGCA 1057
 Qy 757 AAAATGTTCTGTCACCTTGATGTAATGCTGCTCAATTTTATTTTATTTTATTTT 816
 Db 1058 AAAATGTTCTGTCACCTTGATGTAATGCTGCTCAATTTTATTTTATTTTATTTT 1117
 Qy 817 ATCTTGATGTCACCAAAATTCAGAAAATGATCTCTGATGATTTCTGTTTATTTTGG 876
 Db 1118 ATCTTGATGTCACCAAAATTCAGAAAATGATCTCTGATGATTTCTGTTTATTTTGG 1177
 Qy 877 TCATCTTTAAGATGTCAGAAATGTTTAAACAGAAAGAACTTTTCTAAGAAATG 936
 Db 1178 TCATCTTTAAGATGTCAGAAATGTTTAAACAGAAAGAACTTTTCTAAGAAATG 1237
 Qy 937 ATACATGAAAAGATTTTATTTTAAATGAGTTGTAAGCTTTGTTCTTTGTTGCTG 996
 Db 1238 ATACATGAAAAGATTTTATTTTAAATGAGTTGTAAGCTTTGTTCTTTGTTGCTG 1297
 Qy 997 AAGCATCTGCGCAAGTAAATGCAATGACACATTTTATGTCAGAAAACACACACA 1056
 Db 1298 AAGCATCTGCGCAAGTAAATGCAATGACACATTTTATGTCAGAAAACACACACA 1357
 Qy 1057 CAC 1104
 Db 1358 CAC 1405

 RESULT 3
 BD276315 1581 bp DNA linear PAT 17-JUL-2003
 LOCUS BD276315 EXPRESSED IN HIPPOCAMPUS.
 DEFINITION BD276315.1 GI:33086083
 ACCESSION BD276315.1 GI:33086083
 VERSION JP 2002543833-A/1.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 1581)
 Baughn,M.R., Lal,F., Yue,H., Tang,T.Y., Azimzai,Y. and Kaser,M.R.
 MOLECULES EXPRESSED IN HIPPOCAMPUS
 Patent: JP 2002543833-A 1 24-DEC-2002;
 INCYTE GENOMICS INC, Matthew R KASER, Preeti LAL, Henry YUE, Tom Y
 TANG, Mariah R BAUGHN, Yalda AZIMZAI
 COMMENT OS Homo sapiens
 PN JP 2002543833-A/1
 PD 24-DEC-2002
 PR 10-MAY-2000 JP 200618442
 PI 17-MAY-1999 US 09/313300
 PI mariah r baughn, preeti lal, henry yue, tom y tang, yalda azimzai,
 matthew r kaser
 CC This description about <220> can't be interpreted CC <220>
 CC <221> misc feature
 CC <223> incyte ID No.: 239240
 FH Key Location/Qualifiers.
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 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
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 Query Match 71.6%; Score 790; DB 6; Length 1581;
 Best Local Similarity 90.5%; Pred. No. 9.3e-115;
 Matches 985; Conservative 0; Mismatches 70; Indels 33; Gaps 12;
 Qy 48 GCGGAGAGAGGCGCGCGGCGGAGCCCGGAGACGCGACCATGTGGAGTGTCTGCTTAC 107
 Db 1 GCGGAGAGAGGCGCGCGGCGGAGCGCGGAGCGCGACCATGTGGAGTGTCTGCTTAC 59
 Qy 108 GCGGAGAGAGGCGCGCGGCGGAGCGCGGAGCGCGACCATGTGTCTGCTG 167

Db 60 GCGGAGAGAGGCGCGCGGCGGAGCGCGGAGCGCGACCATGTGTCTGCTG 119
 Qy 168 GCGGAGAGAGGCGCGCGGCGGAGCGCGGAGCGCGACCATGTGTCTGCTG 227
 Db 120 GCGGAGAGAGGCGCGCGGCGGAGCGCGGAGCGCGACCATGTGTCTGCTG 179
 Qy 228 GCGGAGAGGCGCGGAGCGCGGAGCGCGGAGCGCGACCATGTGTCTGCTG 287
 Db 180 GCGGAGAGGCGCGGAGCGCGGAGCGCGGAGCGCGACCATGTGTCTGCTG 239
 Qy 288 AAAAATGAGCGCGGAGCGCGGAGCGCGGAGCGCGACCATGTGTCTGCTG 345
 Db 240 AAAAATGAGCGCGGAGCGCGGAGCGCGGAGCGCGACCATGTGTCTGCTG 299
 Qy 346 GAGGAGATGAGGAGCGCGGAGCGCGGAGCGCGGAGCGCGACCATGTGTCTGCTG 405
 Db 300 GAGGAGATGAGGAGCGCGGAGCGCGGAGCGCGGAGCGCGACCATGTGTCTGCTG 359
 Qy 406 TGAATATTTATCTAGCTTGG-TACCGAGAGAAATGACACCTGATCTGCTG-ATG 463
 Db 360 TGAATATTTATCTAGCTTGG-TACCGAGAGAAATGACACCTGATCTGCTG-ATG 419
 Qy 464 CCGGAGAGAGGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCG 521
 Db 420 CCGGAGAGAGGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCG 479
 Qy 522 CAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 566
 Db 480 CAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 539
 Qy 567 -TCCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 621
 Db 540 CAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 599
 Qy 622 CTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 676
 Db 600 CTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 659
 Qy 677 GCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCG 735
 Db 660 GCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCG 719
 Qy 736 TTTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 795
 Db 720 TTTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 779
 Qy 796 TTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 855
 Db 780 TTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 839
 Qy 856 AAGATATCTGTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 915
 Db 840 AAGATATCTGTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 899
 Qy 916 AAGGAGATTTTCTAAGGATGATCAATGAAAGATTTTATTTTAAATGAGTTGTAAG 975
 Db 900 AAGGAGATTTTCTAAGGATGATCAATGAAAGATTTTATTTTAAATGAGTTGTAAG 959
 Qy 976 CTTGTGTTTCTTTGTTGCTGCAAGTATCTGCCAAGTTAATGAAATGAGCAATTTT 1035
 Db 960 CTTGTGTTTCTTTGTTGCTGCAAGTATCTGCCAAGTTAATGAAATGAGCAATTTT 1019
 Qy 1036 TATGTCAAAAAACAA 1095
 Db 1020 TATGTCAAAAAACAA 1079
 Qy 1096 AAAAAAA 1103
 Db 1080 AAAACAAA 1087
 RESULT 4
 AX049462

LOCUS	AX049462	1581 bp	DNA	linear	PAT 12-JAN-2001
DEFINITION	Sequence 1 from Patent WO070036.				
ACCESSION	AX049462				
VERSION	AX049462.1	GI:12226181			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE					
AUTHORS	Kaefer M.R., Lal P., Yue H., Tang Y.T., Baughn, M.R. and Azimzai, Y.				
TITLE	Genes expressed in hippocampus				
JOURNAL	Patent: NO 0070036-A 1993-NOV-2000;				
FEATURES	<p>1 Inctyle Genomics, Inc. (US)</p> <p>Location:Qualifiers</p> <p>1..1581</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="unassigned DNA"</p> <p>/db_xref="taxon:9606"</p> <p>/note="Inctyle ID No.: 239240"</p>				
ORIGIN					
Query Match	71.6%;	Score 790;	DB 6;	Length 1581;	
Best Local Similarity	90.5%;	Pred. No. 9.3e-115;			
Matches 985;	Conservative	0;	Mismatches 70;	Indels 33;	Gaps 12.
QY	48	GGCGGAGAGAGCGCCGCGCGGAGCGCCCGGAGCGGACGACATGTGGAGGTCTGCCCTTAC			107
DB	1	GGCGGAGAGAGCGCGCGCGCGGAG-CCCCGAGCGGACGACATGTCCGAGGTCTGCCCTTAC			59
QY	108	GGCGAGAGAGAGCTGAGCCCTTACCGGACGCGCGGACGAGCGTGGGCGACAGTCTTCTCTCG			167
DB	60	GGCGAGAGAGAGCTGAGCCCTTACCGGACGCGCGGACGAGCGTGGGCGACAGTCTTCTCTCG			119
QY	168	CGCTCGAGAGACCAACAACTTTCTTGGCGCGCGGAGAGACAAACGCGCGCCGACAGCTG			227
DB	120	CGCTCGAGAGACCAACAACTTTCTTGGCGCGCGGAGAGACAAACGCGCGCCGACAGCTG			179
QY	228	GGCGAGATCGCGCGGAGCAAGGGGTTTATTAAGAGATGATGATGATGATGATGATGATGATG			287
DB	180	GGCGAGATCGCGCGGAGCAAGGGGTTTATTAAGAGATGATGATGATGATGATGATGATGATG			239
QY	288	AAATATATGACCAACAAGGACCT-CTGTGTCTAACT-CCCCAAGACATGATGATGATG			345
DB	240	AAATATATGACCAACAAGGACCTCTGTGTCTAACTCCCCAAGACATGATGATGATG			299
QY	346	GGAGGATATGAGAAACGGCGGTACAGTTATGGGAAAGACATGAAAGAGAAAGCACTT			405
DB	300	GGAGGATATGAGAAACGGCGGTACAGTTATGGGAAAGACATGAAAGAGAAAGCACTT			359
QY	406	GGAAATTTATTAAGTGTG-TCGCCAGATGAAATCAACACTGTATCTGTAT-ATG			463
DB	360	GGAAATTTATTAAGTGTGCTTACCGAGATGAAATCAACACTGTATCTGTATCTGTATCTGT			419
QY	464	CCCGGAGACAGATTTAGCGCA-AG			521
DB	420	CCCGGAGACAGATTTAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCT			479
QY	522	CAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA			566
DB	480	CAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA			539
QY	567	-TCCATATTAAGATTAAGAGAGTCTCAGT---GCAATATGGCAAAATTAATTAATTAATTA			621
DB	540	CATATTAAGATTAAGAGAGAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCTC			599
QY	622	CTTTTATTAAGAG---AATATGGCAATTAATTAATTAATTAATTAATTAATTAATTAATTA			676
DB	600	CTTTTATTAAGAGAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCTC			659
QY	677	GGGG-ACCCAGAGTTTGGAGGTTGGAGATCTTGGTGTGGTGTGGTGTGGTGTGGTGTGG			735

Db		660	GCAGCAACACAGGGTGTTTAAGGTGCGCATTCTTCGCTGAATTTTGCGTTCACAAAG	719
Oy		736	TTTACATTTATTTATATCTTGCAAATAATGGTTCTGTGCACTTGGATGTGAAATGCTGACAG	795
Db		720	TTTACATTTATTTATATCTTGCAAATAATGGTTCTGTGCACTTGGATGTGAAATGCTGCCAG	779
Oy		726	TTTTATTTTTTTTAAGTGTGATCCTTGCGATGACAAAAAATTGCAAAAATGATCTCGT	855
Db		780	TTTTATTTTTTTTAAGTGTGATCCTTGCGATGACAAAAAATTGCAAAAATGATCTCGT	839
Oy		856	AGAATATCTGTTTATTTTGGTCACTTTGAAAGTTATCACAGAAATGTGTTTAAACAGA	915
Db		840	AGATATCTGTTTATTTTGGTCACTTTGAAAGTTATCACAGAAATGTGTTTAAACAGA	899
Oy		916	AGAAACTTTTTCAGAGAAATGATCATAGAAAAAGTTTATTTTAAATAGATGTGAAG	975
Db		900	AGAAACTTTTTCAGAGAAATGATCATAGAAAAAGTTTATTTTAAATAGATGTGAAG	959
Oy		976	CTTGTTGTTTCTTTGTTGCTGCAAGCTATCTGCCAAGTTATGCAATGSAACAATTTT	1035
Db		960	CTTGTTGTTTCTTTGTTGCTGCAAGCTATCTGCCAAGTTATGCAATGSAACAATTTT	1019
Oy		1036	TATGTCCAAAAAACGA	1095
Db		1020	TATGTCCAAAAAACGA	1079
Oy		1096	AAAAAAAAA 1103	
Db		1080	AAAAACAA 1087	
RESULT 5				
CQ776764/c				
LOCUS			1321 bp	DNA linear PART 11-MAR-2004
DEFINITION			Sequence 450 from Patent EP1394274.	
ACCESSION			CQ776764	
VERSION			CQ776764.1 GI:45380154	
KEYWORDS			Homo sapiens (human)	
SOURCE			Homo sapiens	
ORGANISM			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE			1 Ohtani N., Sugita Y., Yamaya M., Kubo H., Nagai H. and Izuhara K. Authors Title Methods of testing for bronchial asthma or chronic obstructive pulmonary diseases Journal Patent: BP 1394274-A 450 03 -MAR-2004; Genom Research, Inc. (JPN) Location/Qualifiers Features source 1..1321 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	
ORIGIN				
Query Match			57.3%; Score 632.6; DB 6; Length 1321;	
Best Local Similarity			89.0%; Pred. No. 6..1e-90;	
Matches 816; Conservative 0; Mismatches 69; Indels 32; Gaps 11;				
Oy		220	CCAAGCTGGCCAGATCGCGCGAGCAAGCGGGTGTATTGAAGATGATGAGATTGATG	279
Db		1321	CCAAGCTGGCCAGATCGCGCGAGCAAGCGGGTGTATTGAAGATGATGAGATTGATG	1262
Oy		280	ACGTCGTGAAAATATGACGACAAAGCACTTCTGTCGTAACT--CCCAAAGCAAT	337
Db		1261	ACGTCGTGAAAATATGACGACAAAGCACTTCTGTCGTAACTCCCCAAAGCAAT	1202
Oy		338	GAGTTAAGGAGAGATATGAAACGCGCTTAACGTTATTGCAAAAAAGCATGAAAGAGA	397
Db		1201	GAGTTAAGGAGAGATATGAAACGCGCTTAACGTTATTGCAAAAAAGCATGAAAGAGA	1142
Oy		398	AAGACTTTGAATTTATTAAGCTTG--TACCACGATGAATTCACAAACCTGTATCG	456

Dd		1141	AAGCACTTGGAAATTATTTACTAGCTTCACCCACAATTAATAACAACCTGTATC	1087
Oy		457	GAT-ATCCCGGAGAAGATTAGCGA-AAGAGGAAGAGAAGAAAGCTTG	514
Dd		1081	GATACAGCCCGGAGAGCATGTGGGAGAGAGAGAGAGAGAGAAAGCTCG	1022
Oy		515	C-CCTCTCAAATTTAAAAAAAATTTAAAAATTAATAATCCCTTA-----	566
Dd		1021	CTCTCTCCMAAAATTTTTAAAAATTAATAATTTAAAAATTAATAATTC	962
Oy		567	-----TCCCATAAAGATTTAAAAAGCTCACG---GCAGTATGCCAAATTA	613
Dd		961	TATATACAAATTAAAGAAATTAAGAAGCTCAGTTCAGCTATTGTCAAAATTA	902
Oy		614	ATCCATTTCTTTTAAATACGG---AATATGCAATTATAGTCTGAATTTG-AACC	668
Dd		901	ATCCATTTCTTTTATATACGGGAAATATGCGCAATTATATAGTCTGAATTTGA	842
Oy		669	TTAATGAGCGG-AACCCAGGTGTTTAGGTGGAATTTTCGCTGAATTTGCTGT	727
Dd		841	TTAATGAGCGGAAACAAGAGTTTGAAGTGTGGCAITCTTCGCTGAATTTGCTGT	782
Oy		728	TCCCAATGTTCATTTAATCTTGCMAAAATGTTCTGTGCACTTGATGTGAATG	787
Dd		781	TCCCAATGTTCATTTAATCTTGCMAAAATGTTCTGTGCACTTGATGTGAATG	722
Oy		788	CTGTCACTTTATTTTTTTTANGTTTATCTTGSATGTCGAAGTCAAAAATTCA	847
Dd		721	CTGTCACTTTATTTTTTTTANGTTTATCTTGSATGTCGAAGTCAAAAATTCA	662
Oy		848	ATCTGTAGATTCGTGTTTATTTTSGTATCTTTAGAGTTATCGAAATGCTTA	907
Dd		661	ATCTGTAGATTCGTGTTTATTTTSGTATCTTTAGAGTTATCGAAATGCTTA	602
Oy		908	AAACAAGAGAGAACCTTCTAAGAAATGATATGAAAAATTTTAAAAATGAG	967
Dd		601	AAACAAGAGAGAACCTTCTAAGAAATGATATGAAAAATTTTAAAAATGAG	542
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Dd		541	TTGTAACTTGCTTTCTTTGTGTCGAAGCTATCTGCCAAGTTATGCAATGAC	482
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Dd		481	ACATTTTATGTCAAAAAACAACAACAACAACAACAACAACAACAACAACA	422
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Dd		421	ACGAAAAACAAGAAAA 405	
RESULT 6				
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LOCUS				
DEFINITION		Sequence 3 from Patent WO0212279.		
ACCESSION		AX451461		
VERSION		AX451461.1 GI:21698462		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Eukaryote; Metazoa; Chordata; Gracilata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	Bihain,B., Bour,B. and Bouguenerec,J. Schizophrenia related gene and protein Patent: WO 0212279-A 3 14-FEB-2002;			
AUTHORS	JOURNAL	GENSET (FR)		
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[illegible]

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Db	75843	1	ATGGTCTGGACCTTGGATGTGAAAGCGTGCACAGTTTATTTTTTATATGTTATC							
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Db	75903	1	CTGGATGTGCAAAATATTCAGAAATATGATCTCTGTAATATTTCTGTTATTTGGTCA							
Db	880	1	TCTTTAGAGTTTACGAGATGTGTTTAAACAGACAGAGACCTTTCTAACAGATGATA							
Db	75963	1	TCTTTAGAGTTTACGAGATGTGTTTAAACAGACAGAGACCTTTCTAACAGATGATA							
Db	940	1	CATGAAAAAATTTATTTTAAATGATGTTTAAAGCTGTGTGTTCTTTGTTGTCGACAG							
Db	76023	1	CATGAAAAAATTTATTTTAAATGATGTTTAAAGCTGTGTGTTCTTTGTTGTCGACAG							
Db	76083	1	CTATCTCCCAATTTATGCAAAATGACACATTTTATTTATGCAAAAAACACACACACAC							
Db	1060	1	AC							
Db	76143	1	AC							
RESULT 8	AL391357	195076 bp	linear	PRI 18-MAY-2005						
LOCUS	AL391357									
DEFINITION	Human DNA sequence from clone RP11-401M6 on chromosome 11 contains the gene for calmodulin-dependent protein kinase II (CAMKIIA1), the gene for a non protein (FLJ12875), a ribosomal protein S4 X-linked (RPS4X), pseudogene, the CDA gene for cyclidine deaminase, the PINK1 gene for PTEN induced putative kinase 1, a novel gene (FLJ003877), the DDOST gene for dolichyl-diphosphooligosaccharide-protein glycosyltransferase and the 3' end of the KIF17 gene for kinesin family member 17, complete sequence.									
ACCESSION	AL391357									
VERSION	AL391357.20	GI:16501137								
KEYWORDS	HTG; Camk1a1; CDA; cyclidine deaminase; DDOST; FLJ003877; FLJ12875; KIF17; PINK1; RPS4X.									
SOURCE	Human sapiens									
ORGANISM	Human sapiens									
REFERENCE	Kimberley, A.									
AUTHORS	Direct Submission									
TITLE	Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk									
JOURNAL	On Oct 26, 2001, this sequence version replaced gi:16304938.									
COMMENT	The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WormBase; Information on the WormBase database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormbase This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further Information can be found at http://www.sanger.ac.uk/HGP/Ch1 RP11-401M6 is from the library RPc1-11.2 constructed by the group of Plietser de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBAC3.6									
----- Genome Center										
Center: Wellcome Trust Sanger Institute										
Center code: SC										
Web site: http://www.sanger.ac.uk										

Contact: vegae@anger.ac.uk

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
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RESULT 9	LOCUS	DEFINITION
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		PRI 27-JUN-2005
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		inhibitor 1, mRNA (cDNA clone MGC:22256 IMAGE:4703846), complete

ACCESSION	BC020630
VERSION	BC020630.1
KEYWORDS	GI:18089055
SOURCE	MGC.
ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE
1 (bases 1 to 1377)
Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,
Wolfe, A. P., Bennett, D. C., Bryant, J. D., Chabot, J. C.,

Thu Mar 9 09:22:23 2006

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Page 10

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REFERENCE	1 (bases 1 to 163801)				
AUTHORS	Waterson,R.H.				
TITLE	The sequence of Homo sapiens clone				
JOURNAL	unpublished				
REFERENCE	2 (bases 1 to 163801)				
AUTHORS	Waterson,R.H.				
TITLE	Direct Submision				
COMMENT	Submitted (07-MAR-2000) Genome Sequencing Center, Washington				
	University School of Medicine, 4444 Forest Park Parkway, St. Louis				
	MO 63108, USA				
COMMENT	On Apr 19, 2000 this sequence version replaced gi:7321912.				

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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H NH0004109
----- Summary Statistics -----
Sequencing vector: M13, 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 145820 bases at least Q40
Consensus quality: 150999 bases at least Q30
Consensus quality: 153111 bases at least Q20
Insert size: 185000; agarose-fp
Insert size: 160801; sum-of-contigs
Quality coverage: 3.57 in Q20 bases; agarose-fp
Quality coverage: 4.25 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 31 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
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1641: gap of unknown length
1743: contig of 1703 bp in length
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3444: gap of unknown length
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	*	14159	18450:	contig of 4232 bp in length
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Db	86226	GTGTATTGAAAGATAGATAGATGATTGATGACGTGCTGAAAATAATATGACGCAACAGCACT	86285
Oy	312	CTGCGTGTCAACT-CCCCAAGACAAATAGTTAAGGAGAGAAATGGAAACGGCGGTAA	369
Db	86286	CTGTGTCTCAACTCCCCCAAGACATATGTTAAGGAGAGATTAAGAACGGCGGTAC	86345
Oy	370	AGTTATTGGCAAAAAGCATGAAAAGAAAGACCTTTGAAATTTATTACTACTTG- TAC	428
Db	86346	AGTTATTGGCAAAAAGCATGAAAAGAAAGACCTTTGAAATTTATTACTACTTGCTAC	86405
Oy	429	CCACGATGAATTCACACCTGTATCTGTGTAT-ATGCCCGAGACAGATTAGCGA- AGG	486
Db	86406	CCACGATGAATTCACACCTGTATCTGTGTATCAGCGCGGAGACAGATGAGCGAAGG	86465
Oy	487	AGGAAGAGAGAGAGAGAAAGGCTCTGGGCTCTCTGCAAAAATAAAAATAAAAAAATT	545
Db	86466	AGGAAGAGAGAGAGAGAGAGGCTCTGGGCTCTCTGCAAAAATAAAAATAAAAAAATT	86525
Oy	546	TAAATATATAATCCCTATA- -----TCCCATATAGATTAATAAGATC	589
Db	86526	TAAATATATAATTAATAATAATTCATATATACATATATAAGAAATAAAAAGATC	86585
Oy	590	TCAGT-----GCAGTTTGGCAAAATTAATATCATTTCTTTTAATACGG---AATAT	641
Db	86586	TCAGTTCAGCATTTTGTCAAAATTAATATATTCATTTCTTTTATATACGGTAATTTGC	86645
Oy	642	GGCATTAAGATCTGGAATTTTG-ACACATATATGAAGGGC-ACCCAGGGTTTATAG	699
Db	86646	GCATTAATATAGATCTGGAATTTTGAACCATTAATGAAGGGCAACACAGGTGTTTATAG	86705
Oy	700	TGTTGGCATTTCTGCGATTTGGCTGGTCCCAATGTTACATTATTTATCTTGCAAA	759
Db	86706	TGTTGGCATTTCTGCGATTTGGCTGGTCCCAATGTTACATTATTTATCTTGCAAA	86765
Oy	760	ATGGTTCTGCGACCTTGGATGATGAAATGCTGTCACAGTTTATTTTTTATGTTATC	819
Db	86766	ATGGTTCTGCGACCTTGGATGATGAAATGCTGTCAGTTTATTTTTTATGTTATC	86825
Oy	820	CTTGATGATGCAAAAATTCAGAAATGATCTCTGATATTTCTGTTTATTTGGTCA	879
Db	86826	CTTGATGATGCAAAAATTCAGAAATGATCTCTGATATTTCTGTTTATTTGGTCA	86885
Oy	880	TCTTTAGATTAACAGATATGTTTAAACAGAAAGAGACCTTTCTAAGAAATAT	939
Db	86886	TCTTTAGATTAACAGATATGTTTAAACAGAAAGAGACCTTTCTAAGAAATAT	86945
Oy	940	CATGAAAGAATTTTATTTTAAATAGTGTGAAGGCTGTGTTCTTTGTGCGAG	999
Db	86946	CATGAAAGAATTTTATTTTAAATAGTGTGAAGGCTGTGTTCTTTGTGCGAG	87005
Oy	1000	CTATCTGCCCAAGTTAATGCAATATGAGACATTTTATATGTCAGAAAAACACACACAC	1059
Db	87006	CTATCTGCCCAAGTTAATGCAATATGAGACATTTTATATGTCAGAAAAACACACACAC	87065
Oy	1060	ACACACACACACACACACACACACACGAAAAAATTTTTTTTTTTTTTTT	1104
Db	87066	ACACACACACACACACACACACACACGAAAAAATTTTTTTTTTTTTTTT	87110
RESULT 11			
LOCUS AY204901			
DEFINITION Homo sapiens calmodulin/calmodulin-dependent protein kinase II			
ACCESSION AY204801			
VERSION AY204901.1 GI:30959105			
KEYWORDS Homo sapiens (human)			
SOURCE Organism			
REFERENCE 1 (bases 1 to 860)			

AUTHORS Li N. and Cao X.
TITLE Direct Submission
JOURNAL Submitted (19-DEC-2002) Institute of Immunology, Second Military Medical University, 800 Xiangyin Road, Shanghai, Shanghai 200433, China

FEATURES
source 1 location/Qualifiers
1 860
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="1"
1..860
/gene="CAK1I1alpha"
/note="CAK1I1a"
401..637
/gene="CAK1I1alpha"
/codon_start=1
/product="calcium/calmodulin-dependent protein kinase II inhibitor alpha"
/protein_id="AA049802.1"
/db_xref="GI:30959106"
/translation="MSSEVLPFGDKLSPTGSDGVQGFPSGLQDPTNPFAGQNKRP
PKIQIGRSRVVIEDRIDVLTAKMTDKAPFV"

gene
CDS
10 CAGCGCGCGTGAACCTGTCCGCGCGGCGGAGACCGGCGGAGAGCGCCCGCGCGG 69
324 CACCGCGCGTGAACCTGTCCGCGCGGCGGAGACCGGCGGAGAGCGCCCGCGCGG 383
70 AGCGCGCGGCGGAGACCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 129
384 AGCGCGCGGCGGAGACCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 443
130 AGCGCGCGGCGGAGACCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 189
444 AGCGCGCGGCGGAGACCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 503
DB
190 TCTTCGCGCGCGGCGGAG 249
504 TCTTCGCGCGCGGCGGAG 563
DB
250 GGGTGTGTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 309
564 GGGTGTGTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 623
DB
310 CT-CTGCTGTCTAAGT-CCCCAAGACATGATGATGATGATGATGATGATGATGATGATGAT 367
624 CTCTGCTGTCTAAGT-CCCCAAGACATGATGATGATGATGATGATGATGATGATGATGAT 683
DB
368 ACACTTTTGGCAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 426
684 ACACTTTTGGCAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 743
DB
427 ACCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 485
744 ACCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 803
DB
486 GAGGAG 542
804 GAGGAG 860

ORIGIN

Query Match 39.9%; Score 441; DB 8; Length 860;
Best Local Similarity 93.7%; Pred. No. 9.9e-60; Indels 4; Gaps 4;
Matches 503; Conservative 0; Mismatches 30;

RESULT 12
BD030333 524 bp DNA linear PAT 27-AUG-2002
LOCUS BD030333
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD030333.1 GI:22572075
VERSION BD030333.1
KEYWORDS JP 2001269182-A/6579.

SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Edwards, J.B.D.M., Ducclair, E. and Jordan, J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 6579 02-Oct-2001;
GENSET

COMMENT
OS Homo sapiens (human)
PN JP 2001269182-A/6579
PD 02-Oct-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, BIMERIC DUCCLAIR, JEAN YVES
PI JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40
CC
FH Key location/Qualifiers

FEATURES
source 1..524
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 38.7%; Score 427.2; DB 6; Length 524;
Best Local Similarity 97.8%; Pred. No. 1.5e-57;
Matches 451; Conservative 2; Mismatches 6; Indels 2; Gaps 2;

DB
645 ATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 702
24 ATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 83
DB
703 TGGCATGCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 762
84 TGGCATGCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 143
DB
763 GTTCTGTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 822
144 GTTCTGTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 203
DB
823 GAT 882
204 GAT 263
DB
883 TTAGAGAT 942
264 TTAGAGAT 1002
DB
943 AGAAAGAT 1062
324 AGAAAGAT 1103
DB
1003 TCTGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1062
384 TCTGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1103
DB
1063 CAC 1103
444 CAC 1103

RESULT 13
AX894800 524 bp DNA linear PAT 18-DEC-2003
LOCUS AX894800
DEFINITION Sequence 10663 from Patent EP1033401.
ACCESSION AX894800
VERSION AX894800.1 GI:40049684

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1

AUTHORS Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.

TITLE Expressed sequence tags and encoded human proteins

JOURNAL Patent: EP 1033401-A 10663 06-SEP-2000;

GENSET Genset (FR)

FEATURES

source 1..524

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 38.7%; Score 427.2; DB 6; Length 524;

Best Local Similarity 97.8%; Pred. No. 1.5e-57;

Matches 451; Conservative 2; Mismatches 6; Indels 2; Gaps 2;

QY 645 ATTATGATGCTGATTTTG-ACCACTTAAGAGGCGC-ACCCAGGCTTTGAGCT 702

DB 24 ATTATGATGCTGATTTTGACCACTTAAGAGGCGCAACAGAGTTTGAAGTGT 83

QY 703 TGGCATTTCTGCTGATTTTGCTGCTCCCAATTTTACATTTTAACTTGCAGAAATG 762

DB 84 TGGCATTTCTGCTGATTTTGCTGCTCCCAATTTTACATTTTAACTTGCAGAAATG 143

QY 763 GTTCGTGCTGCTGATTTTGCTGCTCCCAATTTTAACTTGCAGAAATG 822

DB 144 GTTCGTGCTGCTGATTTTGCTGCTCCCAATTTTAACTTGCAGAAATG 203

QY 823 GGATGTCAAAAATTCAGAAAATGATCTCTGATGATATCTGTTTATTTTGGTCACT 882

DB 204 GGATGTCAAAAATTCAGAAAATGATCTCTGATGATATCTGTTTATTTTGGTCACT 263

QY 883 TTAGAGTTATCAGAGATGCTTTTAAACAGAGAGAACTTTCTAGAGATGATATCAT 942

DB 264 TTAGAGTTATCAGAGATGCTTTTAAACAGAGAGAACTTTCTAGAGATGATATCAT 323

QY 943 AGAAAGATTTTATTTTAAATGAGTTGTAAAGCTTGTTTCTTTGCTGCAAGCTA 1002

DB 324 AGAAAGATTTTATTTTAAATGAGTTGTAAAGCTTGTTTCTTTGCTGCAAGCTA 383

QY 1003 TCTGCCCAAGTTAAAGCAATGAGACATTTTAAATGTCAGAAAACACACACACACA 1062

DB 384 TCTGCCCAAGTTAAAGCAATGAGACATTTTAAATGTCAGAAAACACACACACACA 443

QY 1063 CACACACACACACACACACACAGAAAACACACACACACACACACACACACAC 1103

DB 444 CACACACACACACACACACACAGAAAACACACACACACACACACACACACAC 484

RESULT 14

LOCUS BD139338 417 bp DNA linear PAT 18-SEP-2002

DEFINITION Extended cDNA of secretory protein.

ACCESSION BD139338

VERSION BD139338.1 GI:23234283

KEYWORDS JP 2002508182-A/90.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 417)

AUTHORS Bouguetelert, L., Duclert, A. and Edwards, J.B.D.M.

TITLE Extended cDNA of secretory protein

JOURNAL Patent: JP 2002508182-A 90 15-MAR-2002;

GENSET

COMMENT OS Homo sapiens (human)

PN JP 2002508182-A/90

PD 19-MAR-2002

PF 17-DEC-1998 JP 2000539136

PR 17-DEC-1997 US 60/069957,09-FEB-1998 US 60/074121 PR

13-APR-1998 US 60/081563,10-AUG-1998 US 60/096116 PI LYDIE

BOUGUETELERT, AVMERIC DUCLETT, JEAN BAPTISTE DUMAS MILNE PI EDWARDS

PC C12N15/09, C12N15/09, C07K16/47, C07K16/18, C12N1/15, C12N1/19, PC

C12N1/21,

PC C12N5/10, C12P21/02, C12Q1/68, C12N15/00, C12N5/00, C12N15/00, CC

Extended cDNA of secretory protein

Key Location/Qualifiers

FT CDS 327..416

FT polyA site 404..417.

FEATURES

source 1..417

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 36.7%; Score 405.4; DB 6; Length 417;

Best Local Similarity 98.6%; Pred. No. 3.9e-54;

Matches 409; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 690 TGTTCGAGGTGCTGCAATTTCTGCTGATTTGCTGCTCCCAATGTTTACATTTTAA 749

DB 1 TGTTCGAGGTGCTGCAATTTCTGCTGATTTGCTGCTCCCAATGTTTACATTTTAA 60

QY 750 TCTTGCAAAAATGTTCTGCTGCAATTTGCAATTTGCAATTTGCTGCTCCCAATGTTT 809

DB 61 TCTTGCAAAAATGTTCTGCTGCAATTTGCAATTTGCAATTTGCTGCTCCCAATGTTT 120

QY 810 TGTTCGATCTTGGATGATACAAAATTCAGAAAATGATCTCTGATGATTTTCTGTTT 869

DB 121 TGTTCGATCTTGGATGATACAAAATTCAGAAAATGATCTCTGATGATTTTCTGTTT 180

QY 870 ATTTCGATCTTGGATGATACAAAATTCAGAAAATGATCTCTGATGATTTTCTGTTT 929

DB 181 ATTTCGATCTTGGATGATACAAAATTCAGAAAATGATCTCTGATGATTTTCTGTTT 240

QY 930 AGAATATATCATTAAGAAATTTTATTTTAAATGAGTTGTAAGCTTGTTCTTGTG 989

DB 241 AGAATATATCATTAAGAAATTTTATTTTAAATGAGTTGTAAGCTTGTTCTTGTG 300

QY 990 TTGCTGAGAGTATCTGCTGCAAGTTAAAGCAATGAGACATTTTAAATGTCAGAAAAC 1049

DB 301 TTGCTGAGAGTATCTGCTGCAAGTTAAAGCAATGAGACATTTTAAATGTCAGAAAAC 360

QY 1050 AC 1104

DB 361 AC 415

RESULT 15

LOCUS CQ704178 366 bp DNA linear PAT 03-FEB-2004

DEFINITION Sequence 49104 from Patent WO02070737.

ACCESSION CQ704178

VERSION CQ704178.1 GI:42264947

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1

AUTHORS Liew, C.C., Marshall, W.B. and Zhang, H.

TITLE Compositions and methods relating to osteoarthritis

JOURNAL Patent: WO 02070737-A 49104 12-SEP-2002;

Chondrogene Inc. (CA)

FEATURES

source 1..366

Location/Qualifiers

/organism="Homo sapiens"

ORIGIN /mol_type="unassigned DNA"
/db_xref="taxon:3606"

Query Match 31.1%; Score 343.8; DB 6; Length 366;
Best Local Similarity 97.8%; Pred. No. 26-44;
Matches 359; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

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OY 731 CAATGTTTACATTTTAACTCTTGCAAAAATGCTCTGCACTTGATGTAATGCTG 790
Db 1 CAATGTTTACATTTTAACTCTTGCAAAAATGCTCTGCACTTGATGTAATGCTG 60
OY 791 TCCAGTTTATTTTATTTTATGTTGTTATCTTGATGTAACAAAATTCAGAAAATGATC 850
Db 61 TCCAGTTTATTTTATTTTATGTTGTTATCTTGATGTAACAAAATTCAGAAAATGATC 120
OY 851 TCTGTAGATATCTGTTTATTTTGTGATCTTATGAGTTATCGAATGCTGTTAAA 910
Db 121 TCTGTAGATATCTGTTTATTTTGTGATCTTATGAGTTATCGAATGCTGTTAAA 179
OY 911 CAAGAAGAGAACTTTCTAAGAAATGATACATPAGAAAATTTTAAATGAGTTG 970
Db 180 CAAGAAGAGAACTTTCTAAGAAATGATACATPAGAAAATTTTAAATGAGTTG 239
OY 971 TAAAGCTTGTTCTTTGTTGCTGCAAGCTATCTGCCAAGTTAATGCAATGACACA 1030
Db 240 TAAAGCTTGTTCTTTGTTGCTGCAAGCTATCTGCCAAGTTAATGCAATGACACA 299
OY 1031 TTTTATGTCAGAAAAACACACACACACACACACACACACACACACACACAGAAAAA 1090
Db 300 TTTTATGTCAGAAAAACACACACACACACACACACACACACACACACACACAG 359
OY 1091 AAAAAA 1097
Db 360 AAAACA 366

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Search completed: March 9, 2006, 03:30:01
Job time : 5570.2 secs

XX WPI, 2002-241732/29.
DR P-55PB; AME19431.
XX
XX
PT Novel isolated and purified or recombinant polynucleotide encoding PAPAP
PT proein, useful for diagnosing and treating schizophrenia, bipolar
PT disorder and other central nervous system disorders.
XX
XX Claim 2, Page 92; 96pp; English.
XX

CC The invention relates to human PAPAP polypeptides and polynucleotides.
CC The invention also concerns the interaction of PAPAP with schizophrenia.
CC candidate gene g34877. PAPAP polypeptides, gene and anti-PAPAP antibodies
CC are useful for treating schizoprenia, bipolar disorder or related
CC central nervous system (CNS) disorders e.g. psychotic disorders, mood
CC disorders, autism, substance dependence and alcoholism, mental
CC retardation and other psychiatric diseases including cognitive, anxiety,
CC eating, impulse-control and personality disorders. They are also used in
CC vaccines. The present sequence is human PAPAP cDNA. The PAPAP gene is
CC located on chromosome 1p35-p36

SQ Sequence 1104 BP; 350 A; 220 C; 262 G; 272 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1104;	DB 6;	Length 1104;
Best Local Similarity	100.0%;	Pred. No. 3.8e-219;		
Matches 1104; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;

QY	1	GGCAAGAGGACGCGCGCTGACCTCTGTCGCGCGGCGGAGACGCGGCGGAGAGAGCG	60
Db	1	GGCAAGAGGACGCGCGCTGACCTCTGTCGCGCGGCGGAGACGCGGCGGAGAGAGCG	60
QY	61	CGCGGCGGAAACCCCGGAAACGCGACCATGTGGAGGTGTGCGCTTACGAGCGAAGAG	120
Db	61	CGCGGCGGAAACCCCGGAAACGCGACCATGTGGAGGTGTGCGCTTACGAGCGAAGAG	120
QY	121	TGAGCCCTTACGCGAGCGGCGCGAGCGTGGGCGAGATCTTCTCTGCGCGCTGTGAGACA	180
Db	121	TGAGCCCTTACGCGAGCGGCGCGAGCGTGGGCGAGATCTTCTCTGCGCGCTGTGAGACA	180
QY	181	CCAAACAATCTTTCGCGCGCGGCGAGAAACAGCGGCGCGCGAAAGCTGGGCGAGATGGCG	240
Db	181	CCAAACAATCTTTCGCGCGCGGCGAGAAACAGCGGCGCGCGAAAGCTGGGCGAGATGGCG	240
QY	241	GGAGCAAGCGGCTGTATTGAAGATGATAGGATTTGACGTGCTGTAATAATATGACCG	300
Db	241	GGAGCAAGCGGCTGTATTGAAGATGATAGGATTTGACGTGCTGTAATAATATGACCG	300
QY	301	ACAAAGCACTCTGTGTGTCTAACTCCCAAGACAAATGATTAAGGAGAAATAGAAC	360
Db	301	ACAAAGCACTCTGTGTGTCTAACTCCCAAGACAAATGATTAAGGAGAAATAGAAC	360
QY	361	GGCGGTAACTGTTATTTGGCAAAAACATAGAAAAGACACTTTGAAATTTTATCTA	420
Db	361	GGCGGTAACTGTTATTTGGCAAAAACATAGAAAAGACACTTTGAAATTTTATCTA	420
QY	421	GCTTGTACCCACGATGAAATCAAACAACGTGATCTGATTAAGCCCGGAGCAATTAAG	480
Db	421	GCTTGTACCCACGATGAAATCAAACAACGTGATCTGATTAAGCCCGGAGCAATTAAG	480
QY	481	CGAAGAGAGAAAGAGAGAGAAAGAGCTTGGGCGCTGTACAATTAATAATTAATAAAAA	540
Db	481	CGAAGAGAGAAAGAGAGAGAAAGAGCTTGGGCGCTGTACAATTAATAATTAATAAAAA	540
QY	541	AAATTTAAATAATAATAATCCCTAATCCCTATATAATAATAAAGCTCAGTGCAGTA	600
Db	541	AAATTTAAATAATAATAATCCCTAATCCCTAATATAATAATAAAGCTCAGTGCAGTA	600
QY	601	TTGGCAAAATTAATCAATTTCTTTTAATACGGGAATATGGCAATTAAGATCTGGATT	660
Db	601	TTGGCAAAATTAATCAATTTCTTTTAATACGGGAATATGGCAATTAAGATCTGGATT	660
QY	661	TTGACCACTTAATGAGCGGACCCAGAGTATTTGAGGTGTGGCAATCTTCGCTAAT	720

Db	661	TGACCACTTAATGAAGGCGACCCCGAGGTTTGAAGNNTTGACATCTTCGCTGATT	720
Qy	721	TGGGTGTCOCOAATGTTTACATTTATTAATCTTGGCAAAAATGGTCTGGCACTTGGATG	780
Db	721	TGGGTGTCOCOAATGTTTACATTTATTAATCTTGGCAAAAATGGTCTGGCACTTGGATG	780
Qy	781	TGAATCTGTCCAGTTTATTTTTTTTAAATGTTGTATCTTGGATGTCAAAAATTC	840
Db	781	TGAATCTGTCCAGTTTATTTTTTTTAAATGTTGTATCTTGGATGTCAAAAATTC	840
Qy	841	GAATATATCTGTGAGATTTCTGTTTATTTTGGTATCTTGAAGATTCAGAAAT	900
Db	841	GAATATATCTGTGAGATTTCTGTTTATTTTGGTATCTTGAAGATTCAGAAAT	900
Qy	901	GTGTTTAAACAAAGAGAACTTTCTAGAGATGATACATAGAAAAGTTTATTTT	960
Db	901	GTGTTTAAACAAAGAGAACTTTCTAGAGATGATACATAGAAAAGTTTATTTT	960
Qy	961	AAATGAGTTAAACCTGTGTTCTTCTTGTCGTCAGATATGCGCAAGTTATGCA	1020
Db	961	AAATGAGTTAAACCTGTGTTCTTCTTGTCGTCAGATATGCGCAAGTTATGCA	1020
Qy	1021	AATGACACATTTTATATGTGAAAACACACACACACACACACACACACACACAC	1080
Db	1021	AATGACACATTTTATATGTGAAAACACACACACACACACACACACACACACAC	1080
Qy	1081	CACGAAAAAAAAAAAAAAAAAAAA	1104
Db	1081	CACGAAAAAAAAAAAAAAAAAAAA	1104

RESULT 2
AD161702
ID AD161702 standard; cDNA; 1876 BP

DT 22-APR-2004 (first entry)

DE Human cDNA downregulated in Alzheimer's disease, INCYTE 23151.1.
XX
KW Human; ss; Alzheimer's disease; differential display; neuroprotective;
KW brain disorder.

OS Homo sapiens.

PN US6682888-B1.

PD 27-JAN-2004.

PF 05-MAY-2000; 2000US-00566921.

PR 05-MAY-2000; 2000US-00566921.

PA (INCY-) INCYTE CORP.

PI Loring JF, Tingley DW, Edwards CM;

DR WPI; 2004-118572/12.

PT New composition comprising cDNAs that are differentially expressed in

PS Claim 1; SEQ ID NO 70; 223pp; English.

CC The invention relates to a new composition comprising ADI61633-

CC brain disorders. Also included are a high throughput method for detecting

CC nucleic acids and a high throughput method for screening a library of

CC CDNA. The expression of the each of the cDNAs is downregulated at least

CC AD161727) or upregulated at least two fold in Alzheimer's disease
 CC AD161728-AD161770). The composition is useful for diagnosing or treating
 CC Alzheimer's disease. The present sequence is a cDNA downregulated at
 CC least two-fold in the brain of the subjects with Alzheimer's disease.
 XX
 SQ Sequence 1876 BP; 480 A; 442 C; 442 G; 480 T; 0 U; 32 Other;
 Query Match 72.8%; Score 803.8; DB 12; Length 1876;
 Best Local Similarity 87.9%; Pred. No. 8,7e-157;
 Matches 991; Conservative 0; Mismatches 103; Indels 34; Gaps 11;
 QY 10 CAGGCGCGCTGACCTGCTCCGCGCGGAGACCGCGCGGAGAGCGCGCGCGG 69
 DB 279 CAGGCGCGCTGACCTGCTCCGCGCGGAGACCGCGCGGAGAGCGCGCGCGG 338
 QY 70 AGCCCCCGGAGCGGACCATGTGGAGGAGGCGGCTTACGCGGAGAGAGTGAAGCCCT 129
 DB 339 AG-CCCCGAGCGGACCATGTGGAGGAGGCGGCTTACGCGGAGAGAGTGAAGCCCT 397
 QY 130 ACGGCGAGCGGCGGCGGAGCGGCGGCGGAGCGGCGGCGGAGCGGCGGAGCGG 189
 DB 398 ACGGCGAGCGGCGGCGGAGCGGCGGCGGAGCGGCGGCGGAGCGGCGGAGCGG 457
 QY 130 TCTTCCGCGCGGCGGAGCGGCGGCGGAGCGGCGGCGGAGCGGCGGAGCGG 249
 DB 458 TCTTCCGCGCGGCGGAGCGGCGGCGGAGCGGCGGCGGAGCGGCGGAGCGG 517
 QY 250 GCGTTTGTATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 309
 DB 518 GCGTTTGTATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 577
 QY 310 CT-CTGCTGTCTACT-CCCCAAGACATGATGATGATGATGATGATGATGATGAT 367
 DB 578 CTCTGCTGTCTACT-CCCCAAGACATGATGATGATGATGATGATGATGATGAT 637
 QY 368 ACAGTTATTTGGCAAAAAGATGAAAAGAAACATTTGAAATTTTACTGATTTG-T 426
 DB 638 ACAGTTATTTGGCAAAAAGATGAAAAGAAACATTTGAAATTTTACTGATTTGCT 697
 QY 427 ACCACAGATGAATCAACAACCTGTATCTGTAT-ATGCCCGAGAGACATTTAGCGGAG 485
 DB 698 ACCACAGATGAATCAACAACCTGTATCTGTAT-ATGCCCGAGAGACATTTAGCGGAG 757
 QY 486 GAGGAG 545
 DB 758 GAGGAG 817
 QY 546 TAAATTAAT-AAT 586
 DB 818 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 877
 QY 587 GTCTCACT-CCAGATTTGGCAAAAAGATGAAAAGAAACATTTGAAATTTTACTG 640
 DB 878 GTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 937
 QY 641 --TGGCATTTAGATCTGATTTTG-ACCACTTAATGAGCGGC-ACCCGAGGTGTTTG 696
 DB 938 TGGCATTTAGATCTGATTTTGACCACTTAATGAGCGGCACCAAGGTGTTTG 997
 QY 637 AGGTGTGGCAATCTTGGTGAATTTGGCTGTCCCAATGTTTAACTTAATTAATCTTGA 756
 DB 998 AGGTGTGGCAATCTTGGTGAATTTGGCTGTCCCAATGTTTAACTTAATTAATCTTGA 1057
 QY 757 AAAATGTTCTGTGCACTTGAATGAAATGCTGTCACTTTTATTTTATTTATTTGTT 816
 DB 1058 AAAATGTTCTGTGCACTTGAATGAAATGCTGTCACTTTTATTTTATTTATTTGTT 1117
 QY 817 ATCTTGGATGACAAAATTAATGAAATGATCTCTGATGATATCTGTTTATTTTGG 876
 DB 1118 ATCTTGGATGACAAAATTAATGAAATGATCTCTGATGATATCTGTTTATTTTGG 1177
 QY 877 TCATCTTGAAGTTTACGAGATGTGTTTAAACAAGAGAACTTTCTAAGGATG 936

DB 1178 TCATCTTGAAGTTTACGAGATGTGTTTAAACAAGAGAACTTTCTAAGGATG 1237
 QY 937 ATACATGAGAAAAGATTTTATTTTAAATGAGTTGAAAGCTGTGTTTCTTTGTTGCTG 996
 DB 1238 ATACATGAGAAAAGATTTTATTTTAAATGAGTTGAAAGCTGTGTTTCTTTGTTGCTG 1297
 QY 997 AAGCTATCTGCCCAAGTTTATGCAATGACATTTTATGTCAGAAAACACACACCA 1056
 DB 1298 AAGCTATCTGCCCAAGTTTATGCAATGACATTTTATGTCAGAAAACACACACCA 1357
 QY 1057 CAC 1104
 DB 1358 CANGNN 1405
 RESULT 3
 ID AEA43867
 AEA43867 standard; cDNA, 1876 BP.
 XX AEA43867,
 XX 25-AUG-2005 (first entry)
 XX
 XX Human cDNA differentially expressed in brain tissue SEQ ID NO:70.
 XX diagnosis; treatment; brain disease; neuroprotective; cerebroprotective;
 XX muscular-gen.; cytoskeletal; neuroleptic; nootropic; antidepressant;
 XX immunovulant; analgesic; antiparkinsonian; ophthalmological;
 XX immunotherapy; gene therapy; ss.
 OS Homo sapiens.
 XX US2005130171-A1.
 PN 16-JUN-2005.
 PD 26-JAN-2004; 2004US-00765700.
 PF 05-MAY-2000; 2000US-00566921.
 PR (INCY-) INCYTE CORP.
 PA Loring JF, Tingley DW, Edwards CM;
 PI WPI; 2005-456990/46.
 DR
 XX Composition useful for diagnosis, staging, treating or monitoring
 PT treatment of a subject with a brain disorder; comprises several cDNAs
 PT that are differentially expressed in brain disorders.
 XX
 XX Claim 1; SEQ ID NO 70; 231pp; English.
 XX
 CC The invention relates to a composition (I) for the diagnosis, staging,
 CC treatment or for the monitoring of treatment of a subject with a brain
 CC disorder. (I) comprises several cDNAs that are differentially expressed of
 CC in brain disorders and chosen from any one of 138 nucleotide sequences of
 CC AEA43798-AEA43935, or their complements. Also described: (1) a high
 CC throughput method for detecting differential expression of one or more
 CC cDNAs in a sample containing nucleic acids; (2) an isolated cDNA (II)
 CC selected from AEA43812, AEA43813, AEA43830, AEA43855, AEA43856,
 CC AEA43883 and AEA43923; (3) an expression vector (III) containing (II);
 CC (4) a host cell (IV) containing (III); (5) a protein (V) produced using
 CC (IV); and (6) a pharmaceutical composition comprising (V). (I) is useful
 CC for a high throughput method of screening a library of molecules or
 CC compounds to identify a ligand which specifically binds a cDNA, where the
 CC method involves combining (I) with the library of molecules or compound
 CC under conditions to allow specific binding and detecting specific binding
 CC between each cDNA and a molecule or compound. (IV) is useful for
 CC producing a protein, which involves culturing (IV) under conditions for
 CC the expression of the protein and recovering the protein from the
 CC culture. (V) is useful for high throughput method for screening a library
 CC of molecules or compounds to identify a ligand which specifically binds
 CC (V), where the method involves combining (V) or its portion with the

CC library of molecules or compound under conditions to allow specific
 CC binding and detecting specific binding between (V) and a molecule or
 CC compound. (V) is useful for purifying a ligand from a sample, which
 CC involves combining (V) or its portion with the sample under conditions
 CC to allow specific binding, recovering the bound protein and separating the
 CC protein from ligand. (V) is also useful for producing an antibody, which
 CC involves immunizing an animal with (V) or its portion under conditions to
 CC elicit an antibody response, isolating animal antibodies and screening
 CC the isolated antibodies with the protein. (II) is useful in gene therapy
 CC for the treatment or prevention of conditions and disorders associated
 CC with immune response. The present sequence represents a human cDNA
 CC sequence which is differentially expressed in brain tissues, which is
 CC used in the exemplification of the present invention.

SQ Sequence 1876 BP; 480 A; 442 C; 442 G; 480 T; 0 U; 32 Other;

Query Match 72.8%; Score 803.8; DB 14; Length 1876;

Best Local Similarity 87.9%; Pred. No. 8.7e-157;

Matches 991; Conservative 0; Mismatches 103; Indels 34; Gaps 11;

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Qy 10 CAGCGCGCTGACCTGTCGCGCGCGCGGAGACGCGGCGGAGAGAGCGCGCGCGG 69
Db 279 CAGCGCGCTGACCTGTCGCGCGCGCGGAGACGCGGCGGAGAGAGCGCGCGCGG 338
Qy 70 AGCCCCGCGAGCGACCATGTGGAGGTGCTGACCGACGACGAGAACTGAGCCCT 129
Db 339 AG-CCCCGCGAGCGACCATGTGGAGGTGCTGACCGACGACGAGAACTGAGCCCT 397
Qy 130 ACGGCGACGCGCGGCGACGTGGGCGAGATCTTCTGCGCGCGCTGACGACACCAACT 189
Db 398 ACGGCGACGCGCGGCGACGTGGGCGAGATCTTCTGCGCGCGCTGACGACACCAACT 457
Qy 190 TCTTCGCGCGCGCGGAGAACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGC 249
Db 458 TCTTCGCGCGCGCGGAGAACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGC 517
Qy 250 GGGTGTGTTATGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 309
Db 518 GGGTGTGTTATGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 577
Qy 310 CT-CTGCTGCTCACT-CCCCGAAAGACATGTAAGGAGAGAGATGAGACCGCGCTA 367
Db 578 CTCTGCTGCTCACTCCCCGAAAGACATGTAAGGAGAGAGATGAGACCGCGCTA 637
Qy 368 ACAATTATGCGCAAAAGCATGAAAGAGAGACCTTTGAAATTTATTTACTAGCTTG- 426
Db 638 ACAATTATGCGCAAAAGCATGAAAGAGAGACCTTTGAAATTTATTTACTAGCTTGCT 697
Qy 427 ACCCAGATGAAATCAACACTGTATCTGTAT-ATGCCCGAGACAGATTAGCGGAG 485
Db 698 ACCCAGATGAAATCAACACTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCT 757
Qy 486 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 545
Db 758 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 817
Qy 546 TAAATTAAT-----AAATCCTTATATCC-----CATATAGAAATTAAGA 586
Db 818 AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 877
Qy 587 GTCTCAGT---GCAGATTGCGCAAAATTAATCAATTTCTTTTAATACCGGAAAT- 640
Db 878 GTCTCAGTCAAGCTTATTTGTCAAAATTAATTAATTAATTTCTTTTAATACCGGAA 937
Qy 641 --TGSCATTAATAGATCGAGATTTTG-ACCACTTAAGAGAGCGG-ACCCGAGGTTTG 696
Db 938 TGCGCAATTAATAGATCGAGATTTTGACCACTTAATAGAGCGGCAACGAGGTTTG 997
Qy 697 AGGTGTTGGAATCTTCTGCGGATTTGGCTGTGTCGCAATGTTTACATTTAATCTTGA 756
Db 998 AGGTGTTGGAATCTTCTGCGGATTTGGCTGTGTCGCAATGTTTACATTTAATCTTGA 1057
Qy 757 AAAATGTTGTCGACATTTGATGAAATGCTGTCACAGTTTATTTTATGTTGTT 816

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Db 1058 AAAATGTTGTCGACATTTGATGAAATGCTGTCACAGTTTATTTTATGTTGTT 1117
Qy 817 ATCTTGATGATGACAAAATTAATGAGAAATGATCTGTGATGATTTGTTTATTTGG 876
Db 1118 ATCTTGATGATGACAAAATTAATGAGAAATGATCTGTGATGATTTGTTTATTTGG 1177
Qy 877 TCATCTTGAAGATTATCAGAAATGTTTAAACAGAAAGACATTTCTTAAGAAATG 936
Db 1178 TCATCTTGAAGATTATCAGAAATGTTTAAACAGAAAGACATTTCTTAAGAAATG 1237
Qy 937 ATACATGAGAAAGATTTTATTTTAAATGAGTTGTAAGCTTGTGTTCTTGTGTC 996
Db 1238 ATACATGAGAAAGATTTTATTTTAAATGAGTTGTAAGCTTGTGTTCTTGTGTC 1297
Qy 997 AAGCTATCTGCCCAAGTTAATGCAATGAGACATTTTATGTCAGAAAAACACACA 1056
Db 1298 AAGCTATCTGCCCAAGTTAATGCAATGAGACATTTTATGTCAGAAAAACACACA 1357
Qy 1057 CACACACACACACACACACACACACACACACACACACACACACACACACACAC 1104
Db 1358 CAGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1405

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RESULT 4

AAC87358
 AAC87358 standard; cDNA; 1581 BP.

AC87358;
 09-MAR-2001 (first entry)

DE Human developmentally-regulated hippocampus EST, SRO ID NO:1.

KW Human hippocampal gene; hippocampus EST; expressed sequence tag;

KW developmental regulation; drug screening; modulator;

KW expression alteration; Alzheimer's disease; Huntington's disease;

KW schizophrenia; epilepsy; diagnostic probe; gene therapy; neurotropic;

KW neuroprotective; anticonvulsant; neuroleptic; ss.

OS Homo sapiens.

PN WO200070036-A2.

PD 23-NOV-2000.

PF 10-MAY-2000; 2000MO-US013046.

PR 17-MAY-1999; 99US-00313300.

PA (INCY-) INCYTE GENOMICS INC.

PI Kaever MR, Lal P, Yue H, Tang YT, Baughn MR, Azimzai Y;

DR WPI; 2001-016229/02.

PS Claim 2; Page 31; 39pp; English.

The invention relates to novel human developmentally-regulated genes which are expressed in the hippocampus (ESTs given in AAC87358-087364), and to a protein product of a gene of the invention (AAC87358-087364), which are developmentally-regulated hippocampal gene ESTs (expressed sequence tags) were identified on the basis of homology with ESTs (AAC87365-087371) found in adult rat hippocampus but not in foetal rat hippocampus. The invention also relates to expression vectors and host cells comprising a human developmentally-regulated hippocampal gene; recombinant production of the gene product; and a method of screening for a compound which specifically binds to a human hippocampal gene of the invention or its product. It additionally encompasses nucleic acid sequences with at least

PR	30-JUL-1997;	97US-0054234P.
PR	30-JUL-1997;	97US-0054236P.
PR	18-AUG-1997;	97US-0055968P.
PR	18-AUG-1997;	97US-0055969P.
PR	18-AUG-1997;	97US-0055972P.
PR	19-AUG-1997;	97US-0056534P.
PR	19-AUG-1997;	97US-0056543P.
PR	19-AUG-1997;	97US-0056554P.
PR	19-AUG-1997;	97US-0056561P.
PR	19-AUG-1997;	97US-0056727P.
PR	19-AUG-1997;	97US-0056729P.
PR	19-AUG-1997;	97US-0056730P.
XX	(HUMA-) HUMAN GENOME SCI INC.	
FA	Ruben SM, Feng P, Lafleur DW, Moore PA, Shi Y, Kyaw H, Li Y,	
P1	Zheng Z, Carter KC, Endress GA, Wei Y, Fan P, Rosen CA;	
P1	WPI; 1999-153691/13.	
DR	P-PSTDB; AAY00272.	
XX		
PT	New isolated human genes and the secreted polypeptides they encode -	
PT	useful for diagnosis and treatment of e.g. cancers, neurological	
PT	disorders, immune diseases, inflammation or blood disorders.	
PS	Claim 1; Page 217; 312pp; English.	
CC	This sequence represents a nucleic acid molecule which encodes a secreted	
CC	human protein. The gene number is given in the descriptor line. The gene	
CC	can be used to generate fusion proteins by linking to the gene to a human	
CC	immunoglobulin Fc portion (e.g. AAX20403) for increasing the stability of	
CC	the fused protein as compared to the human protein only. The invention	
CC	relates to 81 novel genes and their fragments (nucleic acid sequences);	
CC	AAX20412-x20499; amino acid sequences AXY00258-y00377) which are useful	
CC	for preventing, treating or ameliorating medical conditions e.g. by	
CC	determining the amount of the new polypeptides in a sample or by	
CC	determining the presence of mutations in the new polynucleotides.	
CC	Specific uses are described for each of the 86 polynucleotides, based on	
CC	which tissues they are most highly expressed in (see AAX20412 for	
CC	described uses)	
SQ	Sequence 1510 BP; 473 A; 285 C; 299 G; 450 T; 0 U; 3 Other;	
Query Match	63.4%; Score 699.8; DB 2; Length 1510;	
Best Local Similarity	89.7%; Pred. No. 3.1e-35;	
Matches	893; Conservative 1; Mismatches 69; Indels 33; Gaps 12	
DY	141 GGCGAGGTGGGCGAGATCTTCTCTGCGCGCTGCAGACCAACAATTCTTCGCGC	200
DY	2 GGCGAGGTGGGCGAGATCTTCTCTGCGCGCTGCAGACCAACAATTCTTCGCGC	61
DY	201 GGCGAGACAAACGCCGCCCAAGCGTGGCGAGATCGCGCGAGACGAAGCGGTTGTT	260
DY	62 GGCGAGACAAACGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	120
DY	261 GAGGATGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	319
DY	121 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	180
DY	320 TTAAT-CCCCAAGAAGCAATGATGATGATGATGATGATGATGATGATGATG	378
DY	181 TTAATCCCCCAAGAAGCAATGATGATGATGATGATGATGATGATGATGATG	240
DY	319 CAAAAAGCATGAAAAGAAAGACTTTGAATTATTCAGCTTG-TACCAAGATGA	437
DY	241 CAAAAAGCATGAAAAGAAAGACTTTGAATTATTCAGCTTG-TACCAAGATGA	300
DY	438 ATTCACAACTGTTCTGTTGAT-ATGCCCGAGACAGATTAGCGA-ACGAGAAAGA	495
DY	301 ATTCACAACTGTTCTGTTGAT-ATGCCCGAGACAGATTAGCGA-ACGAGAAAGA	360
DY	496 GAGGAGAAAGAGCTTGAGG-CCTCTACAAATAATTAATTAATTAATTAATTAAT	554

Dd		361	AGGAGGAAAGCGCTCGGGCTCCTCTGCAGAAAATAAAAAATAAAAAATTAAATTAATTTT	420
Oy		555	AAATTCCTCTA-----TCCCATATAGAATAAAAAGGTCAGT---	594
Dd		421	AATAATATATAAATTTCACTATACATACATTAAGAAATATAAAAAGACTCTGATTGA	480
Oy		559	GCAGTATGGCAAAATTAATTCATTTCTTTTATATACGG---ATATTGCAATTAA	650
Dd		481	GCTATTGTCAAATTAATATCTCATTTCTTTATATACGGGAATATGGCAATTATA	540
Oy		651	GATCTGAATTTTG-ACCATTATGAAAGCGC- ACCCCAAGTGTTTAGGTGGCAT	708
Dd		541	GATCTGAATTTTGAACAACCTTAATGAAACGGCAACACAGAGTGTGGAGTGTGGCAT	600
Oy		709	TCTTCGCTGATTTGGCTGTGCCAATGTTTACATTAATTAATCTTGCAGAAAATGATTCG	768
Dd		601	TCTTCGCTGATTTGGCTGTGCCAATGTTTACATTAATTAATCTTGCAGAAAATGATTCG	660
Oy		769	TGCACCTGATGTAAGTAGCTGTCAGATTTATTTTTTATGTTATCTTGAGTGT	828
Dd		661	TGCACCTGATGTAAGTAGCTGTCAGATTTATTTTTTATGTTATCTTGAGTGT	720
Oy		829	ACAAAAAATTCAGAAAAATGATCTCGAGATATTCGTTTATTTTGTGATCTTTAGAA	888
Dd		721	ACAAAAAATTCAGAAAAATGATCTCGAGATATTCGTTTATTTTGTGATCTTTAGAA	780
Oy		889	GTTATCGAGAAATGTTTAAACAAGAAAGAACCTTTCTAAGAAATGATACATAGAAA	948
Dd		781	GTTATCGAGAAATGTTTAAACAAGAAAGAACCTTTCTAAGAAATGATACATAGAAA	840
Oy		949	GATTTATTTTAAAAAGAGTGTAAAGCTGTGTTCTTTGTCGCAAGCTAATCGCC	1008
Dd		841	GATTTATTTTAAAAAGAGTGTAAAGCTGTGTTCTTTGTCGCAAGCTAATCGCC	900
Oy		1009	CAGTTATATCAAAATGACACATTTTATATGTCAGAAAAACACACACACACACACA	1068
Dd		901	CAGTTATATCAAAATGACACATTTTATATGTCAGAAAAACACACACACACACACA	960
Oy		1069	CACACACACACACAGAAAAAATAAAAAAAAAAAAA	1104
Dd		961	CACACACACACACACACACAGAAAAAATAAAAA	996
<hr/>				
RESULT 7				
ADD90210				
Xx	ID	ADD90210	standard; cDNA; 1510 BP.	
Xx	AC	ADD90210;		
Xx	AD	29-JUN-2004	(first entry)	
Xx	DT	Novel human secreted protein CDNA seq id 25.		
Xx	XX	gene therapy; cytostatic; cancer; human; gene; ss.		
Xx	OS	Homo sapiens.		
Xx	PN	US2003199683-A1.		
Xx	PD	23-OCT-2003.		
<hr/>				
Xx	Ff	30-MAR-2001;	2001US-00820649.	
Xx	FR	30-JUL-1997;	97US-0054209P.	
Xx	FR	30-JUL-1997;	97US-0054211P.	
Xx	FR	30-JUL-1997;	97US-0054212P.	
Xx	FR	30-JUL-1997;	97US-0054213P.	
Xx	FR	30-JUL-1997;	97US-0054214P.	
Xx	FR	30-JUL-1997;	97US-0054215P.	
Xx	FR	30-JUL-1997;	97US-0054216P.	
Xx	FR	30-JUL-1997;	97US-0054217P.	
Xx	FR	30-JUL-1997;	97US-0054218P.	
Xx	FR	30-JUL-1997;	97US-0054234P.	

XX 30-JUL-1997; 97US-0054202P.
 PR 30-JUL-1997; 97US-0054211P.
 PR 30-JUL-1997; 97US-0054212P.
 PR 30-JUL-1997; 97US-0054213P.
 PR 30-JUL-1997; 97US-0054214P.
 PR 30-JUL-1997; 97US-0054215P.
 PR 30-JUL-1997; 97US-0054217P.
 PR 30-JUL-1997; 97US-0054218P.
 PR 30-JUL-1997; 97US-0054234P.
 PR 30-JUL-1997; 97US-0054346P.
 PR 18-AUG-1997; 97US-0055968P.
 PR 18-AUG-1997; 97US-0055969P.
 PR 18-AUG-1997; 97US-0055972P.
 PR 19-AUG-1997; 97US-0056534P.
 PR 19-AUG-1997; 97US-0056543P.
 PR 19-AUG-1997; 97US-0056544P.
 PR 19-AUG-1997; 97US-0056545P.
 PR 19-AUG-1997; 97US-0056727P.
 PR 19-AUG-1997; 97US-0056729P.
 PR 19-AUG-1997; 97US-0056730P.
 PR 29-JUL-1998; 98MO-US015949.
 PR 26-JAN-1999; 99US-00236557.
 PR 05-JUN-2001; 2001US-0295558P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Feng P, Lafleur DM, Moore PA, Shi Y, Kyaw H, Li Y;
 PI Zeng Z, Carter KC, Endress GA, Wei Y, Fan P, Rosen CA;
 XX
 DR WPI: 2003-874923/81.
 DR F-PSDB: ADG90120.
 PT Nucleic acids encoding 83 secreted polypeptides, useful for preventing,
 PT diagnosing and treating disorders related to their aberrant expression
 PT and activity.
 XX
 PS Claim 1; SEQ ID NO 25; 308bp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule encoding a
 CC secreted protein that is at least 95% identical to a polynucleotide
 CC fragment of any of the nucleotide sequences listed in table 1A of the
 CC specification, which is hybridizable to the nucleotide sequences, a
 CC polynucleotide encoding a polypeptide (or a polypeptide fragment, domain
 CC or epitope of any of the amino acid sequences) listed in table 1A of the
 CC specification, a polynucleotide which is an (allelic) variant of the
 CC nucleotide sequences listed in the specification, a polynucleotide which
 CC encodes a species homologue of the above amino acid sequences, a
 CC polynucleotide capable of hybridizing under stringent conditions to any
 CC of the above polynucleotides, where the polynucleotide does not hybridize
 CC under stringent conditions to a nucleic acid molecule having a nucleotide
 CC sequence of only A or T residues. Also included are a recombinant vector
 CC comprising the above nucleic acid molecule, making a recombinant host
 CC cell comprising the above nucleic acid molecule, an isolated polypeptide
 CC comprising a sequence that is at least 95% identical to the polypeptide
 CC (or its fragment, domain, epitope, secreted form, (allelic) variant or
 CC homologue) encoded by the above nucleic acid molecule, an isolated
 CC antibody that binds specifically to the above polypeptide, a recombinant
 CC host cell produced by the above method and that expresses the above
 CC polypeptide, making an isolated polypeptide, preventing, treating or
 CC ameliorating a medical condition, diagnosing a pathological condition or
 CC a susceptibility to a pathological condition in a subject, identifying a
 CC binding partner to the above polypeptide, the gene corresponding to the
 CC cDNA sequence given in the specification, and identifying an activity in
 CC a biological assay. The nucleic acid molecule and polypeptide are useful
 CC in diagnosing, preventing, prognosising or treating diseases or disorders
 CC associated with aberrant expression and/or activity of the above
 CC polypeptide, such as neural disorders, immune system disorders, muscular
 CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
 CC disorders, cardiovascular disorders, renal disorders, proliferative
 CC disorders and/or cancers. In particular, these diseases are systemic
 CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis,
 CC thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, aetmia,

CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
 CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
 CC may be used for identifying agonists and antagonists of the
 CC polynucleotide and polypeptide. The present sequence is a cDNA from one
 CC of the 83 disclosed secreted protein genes.
 XX
 SQ Sequence 1510 bp; 473 A; 285 C; 299 G; 450 T; 0 U; 3 Other;
 Query Match 63.4%; Score 699.8; DB 10; Length 1510;
 Best Local Similarity 89.7%; Pred. No. 3,1e-135;
 Matches 893; Conservative 1; Mismatches 69; Indels 33; Gaps 12;
 141 GGCGACGCGGCGCAGATCTTCCCTGCGCGCTGACAGACCAACCACTTCTCGCGCC 200
 2 GGCGACGCGGCGCAGATCTTCCCTGCGCGCTGACAGACCAACCACTTCTCGCGCC 61
 201 GGGCGAAGCAAGGCGCGCGCCCAAGCTGGGCGAGATGCGCGAGCAAGCGGTTTAT 260
 62 GGGCGAAGCAAGGCG 120
 261 GAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 319
 121 GAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
 320 TAACT-CCCCAAGACCAATGATGATGATGATGATGATGATGATGATGATGATG 378
 181 TAACTCCCCAAGACCAATGATGATGATGATGATGATGATGATGATGATGATGATG 240
 379 CAAAAGCATGAAAAGAAAGCACTTGAATTTATTAAGCTTG-TACCACAGATGA 437
 241 CAAAAGCATGAAAAGAAAGCACTTGAATTTATTAAGCTTGCTACCCAGATGA 300
 438 AATCAACAACCTGTATCTGTGT-ATGCCCGAGACAGATTAAGCGA-AGAGAGAGAG 495
 301 AATCAACAACCTGTATCTGTGTATGAGCGCGGAGACAGATGAGCGGAGAGAGAGAG 360
 496 GAGAGAGAGAGAGAGCTGGGC-CCTCTACAAATTAATTAATTAATTAATTAAT 554
 361 AGAGAGAGAGAGAGCTGGGCCTCTCTGCAAAATTAATTAATTAATTAATTAAT 420
 555 AAAAACTCCTATA-----TCCCATTAAGAAATTAAGAGTCAAGT----- 594
 421 AAAAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
 595 GGAGATGAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 650
 481 GGTATTTGTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 540
 651 GATCTGATTTTG-ACCACTTAATTAAGCGGC-ACCCAGGTTTGAAGGTGGCAT 708
 541 GATCTGATTTTGACCACTTAATTAATTAAGCGGCACACAGGTTTGAAGGTGGCAT 600
 709 TCTTGCGATTTGGCTGTCCCAATGTTTAACTTTAACTTTGCAAAAATGAGTCTG 768
 601 TCTTGCGATTTGGCTGTCCCAATGTTTAACTTTAACTTTGCAAAAATGAGTCTG 660
 769 TCCACTTGATGGAATGCTGTCAGTTTATTTTATTTTATTTATTTATTTATTTAT 828
 661 TCCACTTGATGGAATGCTGTCAGTTTATTTTATTTTATTTTATTTATTTATTTAT 720
 829 ACAAAAATTTCAAAAATGATCTGTGAATTTCTTTTATTTTATTTTATTTATTTA 888
 721 ACAAAAATTTCAAAAATGATCTGTGAATTTCTTTTATTTTATTTTATTTATTTA 780
 889 GTTATCAGATGTTTATTTTAAACAAGAGAACTTTTAAAGATGATATAGAGAA 948
 781 GTTATCAGATGTTTATTTTAAACAAGAGAACTTTTAAAGATGATATAGAGAA 840
 949 GATTTTATTTTAAATGATGTTTAAAGCTTTTCTTTTATTTTATTTTATTTATTT 1008
 841 GATTTTATTTTAAATGATGTTTAAAGCTTTTCTTTTATTTTATTTTATTTATTT 900
 1009 CAAGTATATCAAAATGAGACATTTTATTTATTTATTTTATTTATTTATTTATTT 1068


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QY 769 TGCATCTGATGTAATGCTGCTCAAGTTTATTTTATGTTGTTATCTTGATGCT 828
DB 661 TGCATCTGATGTAATGCTGCTCAAGTTTATTTTATGTTGTTATCTTGATGCT 720
QY 829 AAAAAAAAAATGCAAAATGATCTCTGTAGATATCTGTTTATTTTATGCTATCTTGA 888
DB 721 AAAAAAAAAATGCAAAATGATCTCTGTAGATATCTGTTTATTTTATGCTATCTTGA 780
QY 889 GTTATCGAATGATGTTTAAAAAACAAGAGAACTTTTCTAAGATGATACATAGAAAA 948
DB 781 GTTATCGAATGATGTTTAAAAAACAAGAGAACTTTTCTAAGATGATACATAGAAAA 840
QY 949 GATTTTATTTTAAAAATGATGTTAAAGCTGTGTTCTTTGTCGCAAGCTATCTGCC 1008
DB 841 GATTTTATTTTAAAAATGATGTTAAAGCTGTGTTCTTTGTCGCAAGCTATCTGCC 900
QY 1009 CAAGTTAATCAAAATGAGACATTTTATGTCAGAAAAACAACACACACACACACACA 1068
DB 901 CAAGTTAATCAAAATGAGACATTTTATGTCAGAAAAACAACACACACACACACA 960
QY 1069 CACACACACACACACACACACACACACACACACACACACACACACACACACAC 1104
DB 961 CACACACACACACACACACACACACACACACACACACACACACACACACACAC 996

RESULT 10
ADQ24238/c
ID ADQ24238 standard; DNA; 2058 BP.
AC ADQ24238;
AT 26-AUG-2004 (first entry)
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7058.
KW soft tissue sarcoma; cytosolic; gene therapy; vaccine; screening; human;
XX ds.
XX Homo sapiens.
XX MO2004048938-A2.
XX 10-JUN-2004.
XX 26-NOV-2003; 2003WC-US038193.
XX 26-NOV-2002; 2002US-0429739P.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX Aziz N, Ginsburg WM, Zlotnick A;
XX WPI; 2004-441208/41.
XX Early detection of soft tissue sarcoma comprises determining expression
XX of a gene in a first soft tissue sample and a normal soft tissue sample
XX and comparing the gene expression, also useful in treating soft tissue
XX sarcoma.
XX Example 2; SEQ ID NO 7058; 210bp; English.
XX The invention relates to a novel method for detecting soft tissue sarcoma
XX which comprises obtaining a first soft tissue sample from an individual
XX and a normal soft tissue sample from the same or different individual,
XX determining the expression of a gene in both samples and comparing the
XX expression of the gene in both soft tissue samples, where a higher level
XX of protein expression in the first soft tissue sample indicates the
XX presence of soft tissue sarcoma. The method of the invention has
XX cytosolic applications and may be useful for detecting soft tissue
XX sarcoma, possibly via gene therapy or vaccine production. The nucleic
XX acid sequences may be useful in diagnostic and screening applications.
XX The current sequence is that of a human soft tissue sarcoma-upregulated
XX DNA of the invention. The current sequence is not shown within the

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CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 2058 BP; 488 A; 468 C; 405 G; 695 T; 0 U; 2 Other;
Query Match 58.2%; Score 642; DB 12; Length 2058;
Beet. Local Similarity 87.3%; Pred. No. 3.3e-123;
Matches 828; Conservative 0; Mismatches 90; Indels 32; Gaps 11;
QY 177 GACACCAACACTTCTTCGCGCCGCGGACAGAACAGCGCCGCCCAAGCTGGGACATC 236
DB 1873 GAGACAGAAACCTTCGACCTCGCGCCGCGCCGCCGCGGACAGAACAGCTGGGACATC 1814
QY 237 GGCAGAGCAAGCGGGTTGTTTAAAGATGATAGATGATGATGATGATGATGATGATG 296
DB 1813 GGCAGAGCAAGCGGGTTGTTTAAAGATGATGATGATGATGATGATGATGATGATG 1754
QY 297 ACCGACAAAGCACT-CTGGGTCTACT-CCCAAGACATGATGATGATGATGATGATG 354
DB 1753 ACCGACAAAGCACTCTCTGTCTACTCCCAAGACATGATGATGATGATGATGATG 1694
QY 355 AAGAACCGCGGTAAAGTATGCGAAAGACATGAAAGAGAAAGCACTTGAATTTA 414
DB 1693 AAGAACCGCGGTAAAGTATGCGAAAGACATGAAAGAGAAAGCACTTGAATTTA 1634
QY 415 TTACTAGCTTG-TACCAAGATGAATCAACCTGTATCTGTAT-ATGCCCGAGAC 472
DB 1633 TTACTAGCTTGCTAACCAAGATGAATCAACCTGTATCTGTATAGCGCGGAGAC 1574
QY 473 AGATTAGGCA-AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 530
DB 1573 AGATTAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1514
QY 531 TAAAAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 574
DB 1513 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1454
QY 575 AAGATTAAGAGCTCACT-CAAGTATGCGAAATTAATTAATTAATTAATTAATTA 630
DB 1453 AATTAATTAAGAGCTCACTCAAGTATGCGAAATTAATTAATTAATTAATTAATTA 1394
QY 631 ACGGAAATAT-AGCATTAATGATCTGATTTTG-ACCACTTAATGAAGAGG-ACC 684
DB 1393 TACGGTAATATGCGCATTAATGATCTGATTTTGAAACCACTTAATGAAGAGGCA 1334
QY 685 CAGGCTTTTGAAGGTGCGATCTTGCATGATGATGATGATGATGATGATGATGATG 744
DB 1333 CAGGCTTTTGAAGGTGCGATCTTGCATGATGATGATGATGATGATGATGATGATG 1274
QY 745 TTTAATCTGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 804
DB 1273 TTTAATCTGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1214
QY 805 TTTAATGTTGTTATCTTGATGATGATGATGATGATGATGATGATGATGATGATG 864
DB 1213 TTTAATGTTGTTATCTTGATGATGATGATGATGATGATGATGATGATGATGATG 1154
QY 865 GTTTTATTTTGGTCACTTTTAGAATGATGATGATGATGATGATGATGATGATG 924
DB 1153 GTTTTATTTTGGTCACTTTTAGAATGATGATGATGATGATGATGATGATGATG 1094
QY 925 TTTAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 984
DB 1093 TTTAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1034
QY 985 CTTGTTGCTGCAAGCTATCTGCCAAGTTAATGCAATGATGATGATGATGATGATG 1044
DB 1033 CTTGTTGCTGCAAGCTATCTGCCAAGTTAATGCAATGATGATGATGATGATGATG 974
QY 1045 AAAAAACACACACACACACACACACACACACACACACACACACACACACACACAC 1104
DB 973 AAAAAACACACACACACACACACACACACACACACACACACACACACACACACAC 914

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XX WPI; 2004-193155/19.
DR
19

PT Testing for bronchial asthma or chronic obstructive pulmonary disease by
PT comparing the expression level of a marker gene in a biological sample
PT from a subject with the expression level of the gene in a sample from a
healthy subject.

PS Claim 1; SEQ ID NO 450; 241pp; English.

The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (1) a reagent (1) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a method for producing an animal model for bronchial asthma or chronic obstructive pulmonary disease; (6) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, comprising to a portion of the marker gene, a ribosome, a polynucleotide that suppresses the expression of the gene through an RNAi effect or an antibody recognizing a protein encoded by a marker gene; and (7) a DNA chip for testing for bronchial asthma or chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. (1) has respiratory and antiallergic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention.

SQ Sequence 1321 BP; 414 A; 255 C; 236 G; 416 T; 0 U; 0 Other;

Query Match	Score	DB	Length
57.3%	632.6	12	1321

Matches 816; Conservative 0; Mismatches 69;

Matches 816; Conservative 0; Mismatches 69; Indels 32; Gaps 11;

Qy	220	CCAAAGCTGAGGCAAGATCGGCGGACCAAGCGGGTGTGTTATGAAATGATAGATTTGATG	279
Db	1321	CCAAAGCTGAGGCAAGATCGGCGGACCAAGCGGGTGTGTTATGAAATGATAGATTTGATG	1262
Qy	280	ACGTGCTGAAAAATATGACCGACAAGGACCT--CTGGTGTCTAACT--CCGCAAAAGCAAT	337
Db	1261	ACGTGCTGAAAAATATGACCGACAAGGACCTCTGGTGTCTAACTCCCCCAAAAGCAAT	1200
Qy	338	GAGTTAAGGGAGAGAAATAGAAAGCGCGGTAAAGTTATGGCAAAAGCATGAAAAAGAG	397
Db	1201	GAGTTAAGGGAGAGAAATAGAAAGCGCGGTAAAGTTATGGCAAAAGCATGAAAAAGAG	1144
Qy	398	AAGCATTTGAAATTTATATCTAGCTGG--TACCAGATGAAATGCAAAACTGTATCG	456
Db	1144	AAGCATTTGAAATTTATATCTAGCTGTCTACCAAGATGAAATGCAAAACTGTATCTG	1082
Qy	457	GTAATATGCCCGAGACAGATTAGGCCA--AGAGAGAAAGAGAGAGAAAGGCTGGG	514
Db	1081	GTAATAGGCTCGGAGAGACAGATTAGGCCAGAGAGAGAGAGAGAAAGGCTCTGGG	1022
Qy	515	C--CCTCTCAATTAATAATAAAAAAAAAATTTTAAATTAATAATTCCTATA-----	566
Db	1021	CTCTCTGCAAAATTAATAATTAATAATTAATAATTAATAATTAATAATTAATTCAC	962
Qy	567	-----TCCCAATTAAGATTAAGAAGTCTCAGT---GCAGTATGGCAAAATTAA	613
Db	961	TATATATCAATATTAAGAAATTAAGAAGCTCTCAGTGCACATTTGTGCAAAATTAAT	902

[illegible]

XX	RESULT 13
XX	ADN04817/c
XX	ADN04817 standard; cDNA; 1321 BP.
XX	
AC	ADN04817;
DT	01-JUL-2004 (first entry)
XX	
XX	Antipsoriatic cDNA sequence #623.
DE	
XX	de; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
XX	
KW	Hom sapiens.
OS	
XX	WO2004028479-A2.
PN	
XX	
PD	08-APR-2004.
XX	
PP	25-SEP-2003; 2003WO-US030907.
PR	25-SEP-2002; 2002US-0414006P.
XX	
PA	(GETH) GENENTECH INC.
XX	
P1	Boðary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WJ,
P1	Wu TD;
XX	
XX	WPI; 2004-305105/28.
DR	F-PSDB; ADN04818.
XX	
PT	New PNO nucleic acid or polypeptide, useful for preparing a
PT	pharmaceutical composition for diagnosing or treating psoriasis in a
XX	mammal.
XX	
XS	Claim 1; SEQ ID NO 1211; 3069pp; English.

Oy		457	GTAATATGCCCGAGACGAGATTGGGA-AGAGAAGAGAGAGAAAGAGCTTCGG	514
Db		241	GTAATCAGCCCGAGACGATGAGCGAGAGAGAGAGAGAGAGAGAGCTCTGGG	300
Oy		515	C-CCTGCACAATAAATAAAAAAAAAAAAAATTTAAAATTAATTAATCCCAT------	566
Db		301	CTCCTCGCAAAAATAAATAAATAAATAAATAAATAAATTTBBAATAAATAAATTCAC	360
Oy		567	-----TCCCATTAAGATAAATAAGACTGAG----GAGTATGGCAAAATTA	613
Db		361	TATATACATATAAAGAAATBAAAAGAGCTCAGTGCAAGCTATTTGTCAAATTAAT	420
Oy		614	ATTCATTCTTTTTTAATACGG--AAATATGCATTAAGATCGAATTTTG-ACCAC	668
Db		421	ATTCATTCTTTTTTAADAGGAAATATGCGCAATTAAGATCTGAAATTTGAAACAC	480
Oy		669	TTAATGACCGC-ACCCAGGTGTTTAGGTGGCAATCTTGCTGATTTGGCTGT	727
Db		481	TTAATGACCGGCAACACAGGTGTTTAGAGTTGGCAATCTTGCTGATTTGGCTGT	540
Oy		728	TCCCAATGTTACATTAATTAATCTTGCAAAATAGTTCGTGCACCTTGAGTGAATG	787
Db		541	TCCCAATGTTACATTAATTAATCTTGCAAAATAGTTCGTGCACCTTGAGTGAATG	600
Oy		788	CTGCGCAGTTAATTTTTTATGTTGTTATCCTGGATGTACAAAATAATTCAGAAATG	847
Db		601	CTGCGCAGTTAATTTTTTATGTTGTTATCCTGGATGTACAAAATAATTCAGAAATG	660
Oy		848	ATCTGTGATGATATCTGTTTATTTTGGTATCTTTAAGATTAACAGAAATGGTTA	907
Db		661	ATCTGTGATGATATCTGTTTATTTTGGTATCTTTAAGATTAACAGAAATGGTTA	720
Oy		908	AACAGAGAGAACATTTCTTAAGAAAGATACATAGAAAATTTTAAAAATAG	967
Db		721	AACAGAGAGAACATTTCTTAAGAAAGATACATAGAAAATTTTAAAAATAG	780
Oy		968	TTGTAAAGCTGTGTTCTTTTGTGTGACAGTATGCGCAATTAATGCAATGAC	1022
Db		781	TTGTAAAGCTGTGTTCTTTTGTGTGACAGTATGCGCAATTAATGCAATGAC	840
Oy		1028	ACATTTTATATGCAAAAAACACACACACACACACACACACACACACACACGAA	108
Db		841	ACATTTTATATGCAAAAAACACACACACACACACACACACACACACACACAC	900
Oy		1088	AAAAAAAAAAAAAAAAA1104	
Db		901	ACGAAAAACAAAGAAA917	
<hr/>				
RESULT 15				
AAD31053				
XX	ID	AAD31053	standard; DNA; 3189 BP.	
XX	AC	AAD31053;		
DT		18-JUN-2002	(first entry)	
XX	DE	Human PAPAP gene.		
KX		Human; PAPAP protein; schizophrenia candidate gene; g34872 gene;		
KM		schizophrenia; bipolar disorder; central nervous system disorder;		
KV		psychotic disorder; mood disorder; autism; mental retardation;		
KW		pschiatric disease; anxiety disorder; impulse-control disorder;		
KY		eating disorder; cognitive disorder; personality disorder; vaccine;		
KZ		chromosome p15-p16; neuroleptic; antialcohollic; tranquiliser;		
LK		antidepressant; nootropic; antiaddictive; ds.		
OS		Homo sapiens.		
PZ		MO200212279-A2.		
XX		14-FEB-2002.		
XX				

Pf	26-JUL-2001; 2001M0-IB001891.
Pr	07-AUG-2000; 2000U0-0223482P.
Xx	(GERT) GENSET.
Ra	Bihain B, Bour B, Bougueleret L;
Pl	WPI; 2002-241732/29.
Dk	
Ft	Novel isolated and purified or recombinant polynucleotide encoding PAPAP
Eg	protein, useful for diagnosing and treating schizophrenia, bipolar
Pt	disorder and other central nervous system disorders.
Xx	
P5	Disclosure; Page 93-94; 96pp; English.
Xx	
Cc	The invention relates to human PAPAP polypeptides and polynucleotides.
Cc	The invention also concerns the interaction of PAPAP with schizophrenia
Cc	candidate gene g34872. PAPAP polypeptides, gene and anti-PAPAP antibodies
Cc	are useful for treating schizophrenia, bipolar disorder or related
Cc	central nervous system (CNS) disorders e.g. psychotic disorders, mood
Cc	disorders, autism, substance dependence and alcoholism, mental
Cc	retardation and other psychiatric diseases including cognitive, anxiety,
Cc	eating impulse-control and personality disorders. They are also used in
Cc	vaccines. The present sequence is human PAPAP gene located on chromosome
SX	1p35-p36
SQ	Sequence 3189 BP; 691 A; 911 C; 959 G; 628 T; 0 U; 0 Other;
Query Match	55.0%; Score 607.2; DB 6; Length 3189;
Best Local Similarity	89.2%; Prid. No. 6,3e-116;
Matches 787; Conservative	0; Mismatches 63; Indels 32; Gaps 11;
Oy	252 GTTGTTTTCAGATGATAGATTGAAGCTGTCAAAATAATGACCGACAAGCACCT 311
Db	2158 GTTGTTTTCAGATGATAGATTGAAGCTGTCAAAATAATGACCGACAAGCACCT 2217
Oy	312 -CTGGTGTCTAACT-CCCCAAGA-CATGAGTTAAGGAGAGATAGAAA-CGCAGCTAC 369
Db	2218 CTGGTGTCTTACTCCGCCAAGA-CATGAGTTAAGGAGAGATAGAAA-CGCAGCTAC 2277
Oy	370 AGTATTGGCAAAAAAGCANTGAAAAGAAAGAACACTTGAATTATTACTAGCTTG-TAC 428
Db	2278 AGTATTGGCAAAAAGCANTGAAAAGAAAGAACACTTGAATTATTACTAGCTTGTC 2337
Oy	428 CGACGATGAAATTCACAAACCTGTATCTGTAT-ATGCCGGAGACATTAGCCCA-AGG 486
Db	2338 CGACGATGAAATTCACAAACCTGTATCTGTATAGCGCGGAGACATTAGGCGAGAGG 2397
Oy	487 AGGAAGAGAGAGAAAGAAAGGCTTGGGC-CCCTTACAAATTAATAATTAATAAATTT 545
Db	2398 AGGAAGAGAGAGAAAGAAAGGCTCTGGGCTCCCTGCAAAATTAATAAATAATAA 2457
Oy	546 TAAATATATAATCCCTATA-----TCCCATTAAGATAAAGAGTC 589
Db	2458 TAAATATATAATTAATAATTCACATATAACATATAAAGAAATTAAGAAGAGTC 2517
Oy	590 TCAAGT----GCAGTATATGGCAAATTAATTAACATTTCTTTTAATAAGGG---AATAT 641
Db	2518 TCAGTGCACACTATTTGTCACAAATTAATTAATTCATTTCTTTTAATAAGGTGAATTCG 2577
Oy	642 GGCAATTATATATGGAATTTTG-ACCACTAATGAAAGGCG-ACCACAGTGTTTAGG 699
Db	2578 GCATTTATATATGGAATTTTGACCACTTAATGAAAGGCGACACAGAGTGTTTAGG 2637
Oy	700 TGTTGGATTTCTTCGCTGATTTGGCTGTTCACAGTTTACATATTATTAATCTGCAAA 759
Db	2638 TGTTGGATTTCTTCGCTGATTTGGCTGTTCACAGTTTATATATTATCTGCAAAA 2697
Oy	760 ATGTTCTGTGCACTTGAGATGAAATGCTGTCAGTTTATTTTTTATGTTGTTATC 819
Db	2698 ATGTTCTGTGCACTTGAGATGAAATGCTGTCAGTTTATTTTTTATGTTGTTATC 2757

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QY 820 CTTGATGTACAAAAATTCAGAAAATGATCTCTGATATTCGTTTATTTTGTCA 879
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    |||||
QY 880 TCTTAGAAGTATCGAGATGTGTTTAAACAAGAGAACTTTCTAAGAAATGATA 939
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    |||||
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Db 2998 ACACACACACACACACACACACACACACACACACACACACACACACACACAC 3039
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GenCore version 5.1.7
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11: gb_seri11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
C 1	632.6	57.3	1321	4	AP116637 Homo sapi
2	623	56.4	954	7	CN643673 ILLUMIGEN
3	615.6	55.8	945	7	CN803102 ILLUMIGEN
4	614.4	55.7	976	7	CN802133 ILLUMIGEN
5	611.8	55.4	950	7	CN803224 ILLUMIGEN
6	611.2	55.3	954	7	CN846790 ILLUMIGEN
7	610.8	55.3	954	7	CN646555 ILLUMIGEN
8	610.2	55.3	954	7	CN646545 ILLUMIGEN
9	609.6	55.2	951	7	CN647038 ILLUMIGEN
10	608.2	55.1	951	7	CN647038 ILLUMIGEN
11	607.2	55.0	1566	4	CR604926 full-length
12	606.4	54.9	955	7	CN644007 ILLUMIGEN
13	605.4	54.8	954	7	CN803392 ILLUMIGEN
14	599.6	54.3	953	7	CN846019 ILLUMIGEN
15	589.8	53.1	964	7	CN846785 ILLUMIGEN
16	586.6	53.1	955	7	CN805169 ILLUMIGEN
17	581.6	52.7	955	7	CN802272 ILLUMIGEN
18	580.2	52.6	951	7	CN802081 ILLUMIGEN
19	579.8	52.5	1020	7	CN803473 ILLUMIGEN
20	574.8	52.1	944	7	CN803534 ILLUMIGEN
21	574.4	52.0	955	7	CN801854 ILLUMIGEN
22	557.2	50.5	1026	7	CN643857 ILLUMIGEN

23	550.6	49.9	993	7	CN802904 ILLUMIGEN
24	548.8	49.7	956	7	CN805265 ILLUMIGEN
25	542.8	49.2	911	7	CN802110 ILLUMIGEN
26	532.6	48.2	967	7	CN644185 ILLUMIGEN
27	520.8	47.2	967	7	CN641685 ILLUMIGEN
28	515.2	46.7	968	7	CN805606 ILLUMIGEN
29	511.2	46.3	806	7	CN642220 ILLUMIGEN
30	503.4	45.6	1001	7	CN802311 ILLUMIGEN
31	500.4	45.3	1004	7	CN801895 ILLUMIGEN
32	499.6	45.3	983	7	CN803331 ILLUMIGEN
33	496	44.9	890	7	CO645235 ILLUMIGEN
34	489.6	44.3	747	3	BO018543 UI-H-DH1-
35	483	43.8	981	7	CN801823 ILLUMIGEN
36	471.2	42.7	914	7	CO645211 ILLUMIGEN
37	463.2	42.0	819	3	B1553632 603190553
38	447.8	40.6	953	7	CO645289 ILLUMIGEN
39	446	40.4	597	8	W17400 zbl5b10.r1
40	445.2	40.3	661	3	BO000750 UI-H-DH1-
41	444.2	40.2	1083	4	CR606015 full-length
42	440.6	39.9	676	5	BO717126 UI-H-E21-
43	437.4	39.6	931	5	BX419572 BX419572
44	437.4	39.6	695	7	CN428017 170006000
45	435.8	39.5	808	5	BU570962 AGENCOURT

ALIGNMENTS

RESULT 1
AP116637/c
LOCUS AP116637 Homo sapiens PRO1489 mRNA, complete cds.
DEFINITION
ACCESSION AP116637
VERSION AP116637.1 GI:7959775
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
AUTHORS Zhang, C., Yu, Y., Zhang, S., Wei, H., Zhou, G., Ouyang, S., Luo, L., Bi, J., Liu, M. and He, F.
TITLE Functional prediction of the coding sequences of 121 new genes deduced by analysis of cDNA clones from human fetal liver
JOURNAL Unpublished
2 (bases 1 to 1321)
REFERENCE
AUTHORS Zhang, C., Yu, Y., Zhang, S., Wei, H., Zhou, G., Ouyang, S., Luo, L., Bi, J., Liu, M. and He, F.
TITLE Direct Submision
JOURNAL Submitted (24-DEC-1998) Department of Experimental Hematology, Institute of Radiation Medicine, Beijing Taping Road 27, Beijing 100850, P. R. China

FEATURES
source
1..1321
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ORIGIN
Query Match 57.3%; Score 632.6; DB 4; Length 1321;
Best Local Similarity 89.0%; Pred. No. 6.8e-124;

RESULT 2	LOCUS	DEFINITION
CN643673	954 bp	mRNA linear EST 12-MAY-2001
CN643673	954 bp	mRNA linear EST 12-MAY-2001
ILLUMIGEN MCQ 8340	Katzke MMR	Macaca mulatta cDNA clone IBUW-32826
5, similar to Baees 1	to 360 highly similar	to human CankiINaIpha
(Hs.197922), mRNA	sequence.	

ACCESSION	ON643673
VERSION	ON643673.1
KEYWORDS	GI:47154683
SOURCE	EST
ORGANISM	Macaca mulatta (rhesus monkey)
REFERENCE	Macaca mulatta Eukaryotes; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecidae; Cercopithecoinae; Macaca. 1 (bases 1 to 954)
AUTHORS	Magness,C.L., Pellin,P.C., Thomas,M.J., Agy,M.B., Proll,S.C., Fitzgibbon,M., Scheer,C.A., Miner,D.G., Kitzze,M.G. and Iadonato,S.F.
TITLE	Analysis of the Macaca mulatta transcriptome and the sequence divergence between Macaca and human
JOURNAL	Genome Biol. 6 (7), R60 (2005)
PubMed	1598449
COMMENT	Contact: C. Magness

Illumigen Biosciences Inc.
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
 Tel: 2063780400
 Fax: 2063780408
 Email: cmagness@illumigen.com
 Sequenced on 2004.01.05. 805 Q20 bases.
 PCR primers
 FORWARD: CCCTCACTAAAGGGAGCAAAA
 BACKWARD: CACTATAGCGCAATTGGCTA
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FEATURES
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        /dev_stage="adult"
        /lab_host="E. coli SGRP"
        /clone_lib="Katzel_PMBR"
        /note="Organ: Brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
        Site 2: Xho I; Created from Stratus ZAP-cDNA synthesis
        kit (catalog #200400) and ZAP-cDNA Gigapack III Gold
        Cloning Kit (catalog #200450)"

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ORIGIN	Query Match	56.4%;	Score 623;	DB 7;	Length 954;
	Best Local Similarity	87.2%;	Pred. No. 7,3e-122;		
	Matches 831;	Conservative 0;	Mismatches 85;	Indels 37;	Gaps 12;
QY	185	CAACTTCCTGGGGCGGGCGGAGAACAGCGGGCGCCCAAGCTGGGGCCAGATCGGCGGAG	244		
Db	1	CAACTTCCTGGGGCGGGCGGAGAACAGCGGGCGCCCAAGCTGGGGCCAGATCGGCGGAG	60		
QY	245	CAAGCGGGTGTATTGAAGATGATGATGACGTGCTGAAAAAATTGACGACAA	304		
Db	61	CAAGCGGGTGTATTGAAGATGATGATGATGACGTGCTGAAAAAATTGACGACAA	120		
QY	305	GGCAGCTTCTGGTGTCTAACTCCCCAAAGCAATGATTTAAGGAGAGATGAAACGG	362		
Db	121	GGCAGCTTCTGGTGTCTAACTCCCCAAAGCAATGATTTAAGGAGAGATGAAACGG	180		
QY	363	CGGTACAGTTATTGGCAAAAAGCATGAAAAAGAAAGACATTGAAATTTATTCTAGC	422		
Db	181	CGATTAAGTTACTGGCAAAAAGCATGAAAAAGAAAGACATTGAAATTTATTCTAGC	240		
QY	423	TTCGATACCAAGATGAACAACACCTGTATCTGGTATATAGCCCGGAGACAGATTAGG	480		
Db	241	TTCGATACCAAGATGAACAACACCTGTATCTGGTATATAGCCCGGAGACAGATTAGG	300		
QY	481	C-----GAGGAGAGAGAGAGAGAAAGGCTTGGCCCTCTACAAATTTAAATA	533		

301 CGTGAAGAGGAGGAGGAGGAGGCTCTGGCTTCTGCAAAAATTAATTAATTA 360
 534 AAAAAAAAAATTTAA--ATATTAATATCCCTATTC-----CATTAAGAAATA 583
 361 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 420
 584 AGAGTCTCACT---GCAGTATGGCAAAATTAATTCATTTCTTTTAATACGG-- 635
 421 GAACTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 480
 636 AATATGCGCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 693
 481 TATGCGCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 540
 694 TTGAGGTTGGCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 753
 541 TTGAGGTTGGCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 754 GCAAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 813
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 874 TGCTCACTTTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTAT 933
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 934 ATGATTAATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTAT 987
 781 ATGATTAATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTAT 840
 988 TGTGCTGCAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 1047
 841 TGTGCTGCAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 900
 1048 AAC 1100
 901 AAC 953

RESULT 3
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 LOCUS ILUMIGEN MC0 32250 Katze MMR Macaca mulatta cDNA clone
 DEFINITION IBUM:12218 5' similar to Bases 61 to 926 highly similar to human
 CARKIN1alpha (Hs.197922), mRNA sequence.
 CN803102
 ACCESSION CN803102.1 GI:47699078
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Macaca mulatta (rhesus monkey)
 Macaca mulatta
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Cercopithecoidea; Cercopithecinae; Macaca.
 1 (bases 1 to 945)
 MAGNES, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B.,
 Pridl, S.C., Flitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
 Iadonato, S.P.
 Analysis of the Macaca mulatta transcritpome and the sequence
 divergence between Macaca and human
 Genome Biol. 6 (7), R60 (2005)
 15398449
 Contact: C. Magnes
 Illumigen Biosciences Inc.
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
 Tel: 2063780400
 Fax: 2063780408
 Email: cmagnes@illumigen.com
 Sequenced on 2004.04.01. 806 Q20 bases.
 PCR Primers

FORWARD: CCTCACTTAAGGAGACAAA
 BACKWARD: CACTTAAGGAGGAGGCTGA
 Insert Length: 945 Std Error: 0.00
 Plate: C000287 row: A column: 11
 Seq primer: CCTCACTTAAGGAGACAAA
 PolyA-No.

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 /note="Organ: brain; Vector: Uni-ZAP XR; Site 1: Recor I;
 Site 2: Xho I; Created from StrataGene ZAP-cDNA synthesis
 kit (catalog #200400) and ZAP-cDNA Gigapack III Gold
 Cloning Kit (catalog #200450)"

ORIGIN
 Query Match 55.8%; Score 615.6; DB 7; Length 945;
 Best Local Similarity 87.1%; Pred. No. 2.7e-120;
 Matches 823; Conservative 0; Mismatches 85; Indels 37; Gaps 12;

185 CAACTTTCTGGGCGCGCGGAGAAACAAGCGCGCCCAAGCTGGCGCGAGCGGAG 244
 1 CAACTTTCTGGGCGCGCGGAGAAACAAGCGCGCCCAAGCTGGCGCGAGCGGAG 60
 245 CAAAGCGGTTGTTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 304
 61 CAAAGCGGTTGTTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 120
 305 GGCACCT-CTGCTGTCTACT-CCCAAGACATAGATTAAAGGAGAGATTAAGAG 362
 121 GGCACCTCTGCTGTCTACT-CCCAAGACATAGATTAAAGGAGAGATTAAGAG 180
 363 CGTAAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTAT 422
 181 CGATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTAT 240
 423 TTG-TACCAAGATTAATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTAT 480
 241 TTGCACTCCCAATTAATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTAT 300
 481 C-----GAAG 533
 301 CGTGAAG 360
 534 AAAAAAAAAATTTAA--ATATTAATATCCCTATTC-----CATTAAGAAATA 583
 361 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 420
 584 AGAGTCTCACT---GCAGTATGGCAAAATTAATTCATTTCTTTTAATACGGATA 639
 421 GAACTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 480
 640 T---TGCACTTAATTAATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTAT 693
 481 TATGCGCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 540
 694 TTGAGGTTGGCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 753
 541 TTGAGGTTGGCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 754 GCAAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 813
 601 GCAAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 814 GTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 873

Db 661 GTATCTCTGGATGTACAAAAATTCAGATATGATCTCTGAGATATCTGTTTATTT 720
QY 874 TGGCACTTTAAAGTTATTCAGAAATGTGTAAAGAAAGAAAGAAAGAAAGAAAG 933
Db 721 TGGTATCTTTAAAGTTATTCAGAAATGTGTAAAGAAAGAAAGAAAGAAAGAAAG 780
QY 934 ATGATACATGAAAAA-----TTTATTTAAATAGTTGAAGCTGTGTTCTT 987
Db 781 ATGATACATGAAAAAAGAAATCTGTTTATTTAAATAGTTGAAGCTGTGTTCTT 840
QY 988 TGTGCTGCAAGCTATCTGCGCAAGTTAAAGCAATTTTATTTATGCAAAAA 1047
Db 841 TGTGCTGCAAGCTATCTGCGCAAGTTAAAGCAATTTTATTTATGCAAAAA 900
QY 1048 AAC 1092
Db 901 CCAC 945

RESULT 4 976 bp mRNA linear EST 26-MAY-2004
LOCUS CN802133
DEFINITION ILUMIGEN MQ0_37701 Katze MMR Macaca mulatta cDNA clone
IBUW:15099 5' similar to Bases 61 to 972 highly similar to human
CAMK1A1pha (Hs.197922), mRNA sequence.
CN802133
ACCESSION CN802133.1 GI:47698109
VERSION EST.
KEYWORDS Macaca mulatta (rhesus monkey)
SOURCE Macaca mulatta
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.
1 (bases 1 to 976)
Magness,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,
Prohl,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and
Iadonato,S.P.
Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human
Genome Biol. 6 (7), R60 (2005)
15998449
Contact: C. Magness
llumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@llumigen.com
Sequenced on 2004.05.17. 751 Q20 bases.
PCR Primers
FORWARD: CCTCCTCAAGGAGGACAAAG
BACKWARD: CACTATGCGCGCAATTTGGGTA
Insert length: 976 Std Error: 0.00
Plate: CL000204 row: F column: 06
Seq primer: CCTCCTCAAGGAGGACAAAG
PolyA-ies.

TITLE
JOURNAL
PUBMED
COMMENT
FEATURES
SOURCE

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/clone="IBUW:15099"
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Site 2: Xho I; Created from Stratagene ZAP-CDNA synthesis
kit (Catalog #200400) and ZAP-CDNA Gispack III Gold
Cloning Kit (Catalog #200450)"

ORIGIN
Query Match 55.7%; Score 614.4; DB 7; Length 976;

Best Local Similarity 86.6%; Pred. No. 4.9e-120; Indels 37; Gaps 12;
Matches 826; Conservative 0; Mismatches 91;

QY 185 CAATCTTTCG 244
Db 1 CAATCTTTCG 60
QY 245 CAAGCGGGTGTATTTGAAGATGATGATGATGATGATGATGATGATGATGATGAT 304
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QY 363 CGGTACAGTTATTTGCAAAAAAGCATGAAAAAGCACTTGAATTTATTTACTAGC 422
Db 181 CGATTAAGTTATTTGCAAAAAAGCATGAAAAAGCACTTGAATTTATTTACTAGC 240
QY 423 TTG-TACCAAGATGAAATCAACAACCTGATCTGAT-ATGCCGAGACAGATTAG 480
Db 241 TTGTTACCAAGATGAAATCAACAACCTGATCTGATCTGATCTGATCTGATCTGAT 300
QY 481 C-----GAAGGAG 533
Db 301 CGTGAAG 360
QY 534 AAAAAAAATTTAA--ATATTAATCCCTATATCC-----CATTAAGATTA 583
Db 361 TAAATTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 420
QY 584 AAGAGCTAGT---GAGATATGCAAAATTAATTCATTTCTTTTATAGAGG---- 635
Db 421 GAAGCTAGTATGAGATTTGTCAAAATTAATTCATTTCTTTTATAGAGGTTAA 480
QY 636 AATATGCAATTAATGATCTGATTTGA--CACTTAATGAAGGCG-ACCAGAGGT 693
Db 481 TATGCGCAATTAATGATCTGATTTGA--CACTTAATGAAGGCGCAACGAGTAT 540
QY 694 TTGAGGTGTCGACTTTTTCGCGATTTGCGTTCGCGATTTGCGTTCGCGATTTGCG 753
Db 541 TTGAGGTGTCGACTTTTTCGCGATTTGCGTTCGCGATTTGCGTTCGCGATTTGCG 600
QY 754 GCAAAATGTTCTGTCGACTTGCATTTGAATGCTGCAAGTTATTTTATGCTT 813
Db 601 GCAAAATGTTCTGTCGACTTGCATTTGAATGCTGCAAGTTATTTTATGCTT 660
QY 814 GTTATCTTGTGATGACAAAATTTCAAAAATGATCTCTGATGATTTCTGTTATTT 873
Db 661 GTTATCTTGTGATGACAAAATTTCAAAAATGATCTCTGATGATTTCTGTTATTT 720
QY 874 TGTGATCTTTAAGAGTTATCAGAAATGTGTAAACAGAAAGAAAGAAAGAAAG 933
Db 721 TGTGATCTTTAAGAGTTATCAGAAATGTGTAAACAGAAAGAAAGAAAGAAAG 780
QY 934 ATGATACATGAAAAA-----TTTATTTAAATGAGTTGAAGCTGTGTTCTT 987
Db 781 ATGATACATGAAAAAAGAAATCTGTTTATTTAAATGAGTTGAAGCTGTGTTCTT 840
QY 988 TGTGCTGCAAGCTATCTGCGCAAGTTAAAGCAATTTTATTTATGCAAAAA 1047
Db 841 TGTGCTGCAAGCTATCTGCGCAAGTTAAAGCAATTTTATTTATGCAAAAA 900
QY 1048 AAC 1101
Db 901 AAC 954

RESULT 5 953 bp mRNA linear EST 26-MAY-2004
LOCUS CN803224
DEFINITION ILUMIGEN MQ0_32542 Katze MMR Macaca mulatta cDNA clone
IBUW:13763 5' similar to Bases 61 to 897 highly similar to human

PCR Primers
 FORWARD: CCTCCTCAATAAGGACAAAA
 BACKWARD: CACTATAGGCGCAATGGGTA
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 Plate: C1000143 row: C column: 01
 Seq primer: CCTCCTCAATAAGGACAAAA
 POLYA=Yes.

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 Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
 kit (Catalog #200400) and ZAP-CDNA Gigapack III Gold
 Cloning Kit (Catalog #200450)"

ORIGIN

Query Match 55.4%; Score 611.2; DB 7; Length 950;
 Best Local Similarity 87.3%; Pred No. 2.4e-119;
 Matches 829; Conservative 0; Mismatches 83; Indels 38; Gaps 13;

185 CACTTCTTGGGGCGGGGAGACAAACGGCCCGCCAGCTGGCCGATCGCGCGAG 244
 1 CACTTCTTGGGGCGGGGAGACAAACGGCCCGCCAGCTGGCCGATCGCGCGAG 60
 245 CAAGCGGGTGTATTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 304
 61 CAAGCGGGTGTATTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
 305 GGCACCTTCTGGTGTCTAACT-CCCAAGCAATGATGATGATGATGATGATGATGATGAT 362
 121 GGCACCTTCTGGTGTCTAACTCCCAAGCAATGATGATGATGATGATGATGATGATGATGAT 180
 363 CGGTAAAGTATTGGCAAAAGCATGAAAGAGAAAGCATTTGAAATTTTACTAGC 422
 181 CGATTAACAGTTACTGGCAAAAGCATGAAAGAGAAAGCATTTGAAATTTTACTAGC 240
 423 TTG-TACCCAGATGAATCAACAACCTGATCTGTAT-ATGCCCGAGACAGATTAGG 480
 241 TTGTAACCAAGATGAATCAACAACCTGATCTGTATAGGCGGAGACAGATTAGG 300
 481 C-----GAG 533
 301 CGTGAAG 360
 534 AAAAAAAAAATTTTAA---ATAATAATCCCTATATCC-----CATATAAATAAA 583
 361 TAAATTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
 584 AAGAGCTCACT----GAGATATGGCAAAATTAATTAATTAATTTTAAATGGAATA 639
 421 GAAGTCAAGTTCAGATATTGTCAAAATTAATTAATTTTAAATTAATTAATTAATTAAT 480
 640 TT-----GGCATTAATGATCTGATTTTG-ACCACTTAATGAGCGGC-ACCCAGGTTT 693
 481 TATTCGCAATTAATGATCTGATTTTGAACCACTTAATGAGCGGCACACGATATT 540
 694 TTGAGGTGTGGCAATTTTGGCTGATTTGGCTGTTCCAAATGTTTAACTTTTAACTTT 753
 541 TTGAGGTGTGGCAATTTTGGCTGATTTGGCTGTTCCAAATGTTTAACTTTTAACTTT 600
 754 GCAAAATATGTTCTGTGCACTTGGATGTAATCTGTCCAGTTTATTTTATTTATGTT 813
 601 GCAAAATATGTTCTGTGCACTTGGATGTAATCTGTCCAGTTTATTTTATTTATGTT 660
 814 GTTATCTTGGATGTAACAAAAATTCAGAAATGATCTGTGATATATCTGTTTATTT 873

Db 661 GTTATCTTGGATGTAACAAAAATTCAGAAATGATCTGTGATATATCTGTTTATTT 720
 Qy 874 TGGTCATCTTTAAGAGTTATCAGAAATGTTTAAACAAAGAGAACTTTTCTAAGA 933
 Db 721 TGGTCATCTTTAAGAGTTATCAGAAATGTTTAAACAAAGAGAACTTTTCTAAGA 780
 Qy 934 ATGATACATAGAAAAA-----TTTTATTTAAATGAGTTTAAAGCTGTGTCTT 987
 Db 781 ATGATACATAGAAAAAAGATCTCTGTTTATTTTAAAGAGTTTAAAGCTGTGTCTT 840
 Qy 988 TGTTCGCAAGCTATCTGCGCAAGTTAATGCAATGACACATTTTATGTCAGAAA 1047
 Db 841 TGTTCGCAAGCTATTTTGGCCAAAGTTAATGCAATGACACATTTTATGTCAGAAC 900
 Qy 1048 AC 1097
 Db 901 ACACACACACACACAC-CCACACACACACACACACACACACACACACACACACAC 949

RESULT 7
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 ILLUMIGEN MCO 26531 Katze MMR Macaca mulatta cDNA clone IBIUM:8439
 5' similar to bases 1 to 360 highly similar to human Cankit1Na1pha
 (hs197922), mRNA sequence.
 CNE46555
 CNE46555.1 GI:47159998

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Macaca mulatta (rhesus monkey)
 Macaca mulatta
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Cercopithecoidea; Cercopithecinae; Macaca.

REFERENCE
 1 (bases 1 to 954)
 Prohl,S.C., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,
 Proll,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and
 Iadonato,S.P.
 Analysis of the Macaca mulatta transcriptome and the sequence
 divergence between Macaca and human
 Genome Biol. 6 (7), R60 (2005)
 15998449

TITLE
 JOURNAL
 PUBMED
 COMMENT

Contact: C. Magness
 Illumigen Biosciences Inc.
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
 Tel: 2063780400
 Fax: 2063780408
 Email: cmagness@illumigen.com
 Sequenced on 2004.03.10. 788 Q20 bases.

PCR Primers
 FORWARD: CCTCCTCAATAAGGACAAAA
 BACKWARD: CACTATAGGCGCAATGGGTA
 Insert Length: 954 Std Error: 0.00
 Plate: C1000144 row: H column: 08
 Seq primer: CCTCCTCAATAAGGACAAAA
 POLYA=Yes

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 /clone="IBIUM:8439"
 /sex="female"
 /dev_stage="adult"
 /lab_host="E. coli SOLR"
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 /note="Organ: brain; Vector: Uni-ZAP XR; Site: 1; Ecor I;
 Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
 kit (Catalog #200400) and ZAP-CDNA Gigapack III Gold
 Cloning Kit (Catalog #200450)"

ORIGIN

[illegible]

ACCESSION	Hs197822	GI:47159688
VERSION	CN646445	
KEYWORDS	CN646445.1	GI:47159688
SOURCE	EST	
ORGANISM	Maca mulatta (rhesus monkey)	
REFERENCE	Maca mulatta	
AUTHORS	Bukacinski, M.; Korth, M.J., Agre, M.B., Mammali, E.; Buitrago, E.; Buitrago, J.L.; Cecchi, P.; Buitrago, J.L.; Buitrago, J.L.	
TITLE	Analysis of the Macaca mulatta transcriptome and the sequence divergence between Macaca and human	
JOURNAL	Genome Biol. 6 (7), R60 (2005)	
PUBMED	15994449	
COMMENT	Contact: C. Magnus Illumigen Biosciences Inc. 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA Tel: 2063780400 Fax: 2063780408 Email: cmagnus@illumigen.com Sequenced on 2004.03.09. 788 Q20 bases. PCR Primers FORWARD: CCTCACTTAAGGACAAACA BACKWARD: CACTATAAGGCGAATGGGT Insert Length: 954 Std Error: 0.00 Plate: Clon00118 Row: D Column: 02 Seq primer: CCCACCTTAAAGGAACAAA POLYA=Yes	
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	/sex="female"	
	/dev_stage="adult"	
	/lab_host="R. coli SOLR"	
	/clone_1b="Katzel-MMBR"	
	/note="Organ: brain; Vector: Uni-ZAP XR; Site: 1; Ecot I; Site 2: Xho I; Created from StrataGene ZAP-CDNA synthesis kit (catalog #200400) and ZAP-CDNA GigaPack III Gold Cloning Kit (Catalog #200450)"	
ORIGIN		
Query Match	55.3%; Score 610.2; DB 7; Length 954;	
Best Local Similarity	86.4%; Pred. 3.8e-119;	
Matches 823; Conservative	0; Mismatches 33; Indels 37; Gaps 12;	
OY	185 CAACCTCTTGCGGCGCGGCAGAACGACGCGCGCCCAAGTCGTGCGCAGATCGCGCGGAG	244
Db	1 CAACCTCTTGCGGCGCGGCAGAACGACGCGCGCCCAAGTCGTGCGCAGATCGCGCGGAG	60
OY	245 CAAGCGGCGGTATTGAAGAGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAG	304
Db	61 CAAGCGGCGGTATTGAAGAGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAG	120
OY	305 GGACACT CTGTGTCTAACT CCCCAAACATAGAGTTAAGGAGAGATAGAAACG	362
Db	121 GGACACTCTGTGTCTAACTCCCCCAAACATAGAGTTAAGGAGAGATAGAAACG	180
OY	363 CGGTAAAGTATATGCAAAAAGCATGAAGAAGAACCTTGAATATTTATTTATAC	422
Db	181 CGATTAACGTTATCGGCAAAAAGCATGAAGAAGAACCTTGAATATTTATTTATAC	240
OY	423 TTG-TACCACAGATGAATCAACAACCTGTATCTGTAT-ATGCCCGAGACAGATTAG	480
Db	241 TTGCTACCAACAGATGAATCAACAACCTGTATCTGTATACGAGCGGAGAGACAGATTAG	300

QY 814 GTTATCTCTGATGTCACAAAATTCAGAAAATGATCTGTAGATATTCGTTTATTT 873
 Db 661 GTTATCTCTGATGTCACAAAATTCAGAAAATGATCTGTAGATATTCGTTTATTT 720
 QY 874 TGGTCATCTTTAGAAAGTTATCAGAAATGCTTTTAAAAACAAGAAAGAACTTTCTAAGA 933
 Db 721 TGGTCATCTTTAGAAAGTTATCAGAAATGCTTTTAAAAACAAGAAAGAACTTTCTAAGA 780
 QY 934 ATGATACATGAAAAAGA-----TTTATTTTAAATGAGTTGTAAGCTTGTTCTT 987
 Db 781 ATGATACATGAAAAAGAATCTGTTTATTTTAAATGAGTTGTAAGCTTGTTCTT 840
 QY 988 TGTGTCGCAAGCTATCTGCCAAGTTATGCAATGACACATTTTATGTCAGAAAA 1047
 Db 841 TGTGTCGCAAGCTATCTGCCAAGTTATGCAATGACACATTTTATGTCAGAAAA 900
 QY 1048 AAC 1101
 Db 901 AAC 951

RESULT 10
 CN647038 951 bp mRNA linear EST 13-MAY-2004
 LOCUS ILLUMIGEN MQ0 27621 Katze JM8R Macaca mulatta cDNA clone IRTM:8006
 DEFINITION 5' similar to Bases 1 to 360 highly similar to human CANKIT1Alpna
 Hs197922), mRNA sequence.
 CN647038
 VERSION CN647038.1 GI:47160481
 KEYWORDS EST.
 SOURCE Macaca mulatta (rhesus monkey)
 ORGANISM Macaca mulatta
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Cercopithecoidea; Cercopithecinae; Macaca.
 1 (bases 1 to 951)
 Magnese,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,
 Prohl,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and
 Iadonato,S.P.
 Analysis of the Macaca mulatta transcriptome and the sequence
 divergence between Macaca and human
 Genome Biol. 6 (7), R60 (2005)
 1598449
 Contact: C. Magnese
 Illumigen Biosciences Inc.
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
 Tel: 2063780400
 Fax: 2063780408
 Email: cmagnese@illumigen.com
 Sequenced on 2004.03.19. 778 Q20 bases.
 PCR Primers
 FORWARD: CCTCACTAAGGGAACAAA
 BACKWARD: CACTATAGGGGAATGGGTA
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 /sex="female"
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 /clone_lib="Katze JM8R"
 /note="Organ: Brain; Vector: Uni-ZAP XR; Site 1: Ecor I;
 Site 2: Xho I; Created from Stragene ZAP-CDNA Synthesis
 kit (catalog #200400) and ZAP-CDNA Gispack III Gold
 Cloning Kit (Catalog #200450)"

ORIGIN

Query Match 55.1%; Score 608.2; DB 7; Length 951;
 Best Local Similarity 86.3%; Pred. No. 1e-118;
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 Db 1 CAATCTTCTGGCGCGCGGAGACACAGCGCGCGCGCAAGCTGGGCGCAGATCGCGCGAG 60
 QY 245 CAAGCGGCTGTTATGTAAGATGATAGATGATGATGATGATGATGATGATGATGATGAT 304
 Db 61 CAAGCGGCTGTTATGTAAGATGATAGATGATGATGATGATGATGATGATGATGATGAT 120
 QY 305 GGCACCT-CTGGTCTTAACT-CCCCAAGACATGATGATGATGATGATGATGATGATGAT 362
 Db 121 GGCACCTCTGGTCTTAACTCCCCAAGACATGATGATGATGATGATGATGATGATGATGAT 180
 QY 363 CGGTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 422
 Db 181 CGATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 QY 423 TTG-TACCGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 Db 241 TTGTCACCGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 QY 481 C-----GAGGAGGAG 533
 Db 301 CGTGAAG 360
 QY 534 AAAAAAAAAATTTAA--ATATTAATTCCTATATCC-----CATTAAGAAATTA 583
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 QY 640 TT-----GGCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 693
 Db 481 TATGCGCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
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 QY 1048 AAC 1098
 Db 901 AAC 951

RESULT 11
 CR604926 1566 bp mRNA linear HTC 21-JUL-2004

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DEFINITION full-length cDNA clone CSDF038YH05 of Fetal brain of Homo sapiens
(human)
ACCESSION CR604326
VERSION CR604326.1 GI:50485733
KEYWORDS HTG, CNS/FT, CDNA
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE 1. Bases 1 to 1566
AUTHORS Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.
TITLES Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1566)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLES Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail: sequef@genoscope.cns.fr
COMMENT - Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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Best Local Similarity 89.2%; Pred. No.1-88-118;
Matches 787; Conservative 0; Mismatches 63; Indels 32; Gaps 11;
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QY 279 GTTGTATTGAAGATATAGATTGATGACGCTGTGAAATATATACCGAAGGACCGCT 338
Db |||||
QY 312 -CTGGTGCTTACCT-CCCCAAGACATGAGTTAAGGAGAGAAATGAGAACGGCGGTAC 369
Db |||||
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Db |||||
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DEFINITION (hs.197922), mRNA sequence.
ACCESSION CN644007
VERSION CN644007.1 GI:47157450
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecoidea; Cercopithecoidea; Macaca.
            1 (bases 1 to 955)
            Magnus, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B.,
            Iadonato, S.P., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
            Analysis of the Macaca mulatta transcriptome and the sequence
            divergence between Macaca and human
            Genome Biol. 6 (7), R60 (2005)
            1598449
            Contact: C. Magnus
            Illumigen Biosciences Inc.
            2203 Airport Way S, Suite 450 Seattle, WA 98134, USA
            Tel: 206780400
            Fax: 2063780408
            Email: cmagnus@illumigen.com
            Sequenced on 2004.01.21. 792 Q20 bases.
            FOR PRIMERS: CCTTCACTTAAGGACAAATAA
            FORWARD: CACTATAGGCGCAATTTGGATA
            BACKWARD: CACTATAGGCGCAATTTGGATA
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DEFINITION      ILUMIGEN MC0_25338 Katze MMR Macaca mulatta cDNA clone
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ACCESSION      CN646019
VERSION      CN646019.1 GI:47159462
KEYWORDS      EST.
SOURCE      Macaca mulatta (rhesus monkey)
ORGANISM      Macaca mulatta
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                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Cercopithecoidea; Cercopithecinae; Macaca.
REFERENCE      1 (bases 1 to 953)
                Magnus, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B.,
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TITLE
JOURNAL
PUBMED
COMMENT

Analysis of the Macaca mulatta transcripome and the sequence
divergence between Macaca and human
Genome Biol. 6 (7), R60 (2005)
1598443
Contact: C. Magnus
illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagnus@illumigen.com
Sequenced on 2004.03.04. 791 Q20 bases.
PCR Primers
FORWARD: CCTCCTACTAAAGGAAACAAA
BACKWARD: CACTATAGGGCGAATTTGGTA
Insert Length: 953 Std Error: 0.00
Plate: CL000117 row: G column: 04
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POLY-A=Yes.

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location/Qualifiers
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/clone="IBTUM:10835"
/sex="female"
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/lab_host="E. coli SOLR"
/note="Organ: brain; Vector: Uni-ZAP XR; Site 1: Bcor I;
Site 2: Xho I; Created from strategene ZAP-cDNA synthesis
kit (catalog #200400) and ZAP-cDNA GigaPack III Gold
Cloning Kit (catalog #200450)"

ORIGIN

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Query Match      54.3%; Score 599.6; DB 7; Length 953;
Beet Local Similarity 85.7%; Pred. No. 6.9e-117;
Matches 816; Conservative 0; Mismatches 99; Indels 37; Gaps 12;

Qy      185 CAACCTTCGCGCGCGGGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 244
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Qy      245 CAAGCGGCTGTGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 304
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Qy      305 GGCACCT-CTGGTCTTAAT-CCCCAAGCAATGATTAAGAGAGAGAGAGAGAGAGAGAGAG 362
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Qy      534 AAAAAAAAAATTTAA--ATAATAAAATCCCTATATCC-----CATATAGAAATAAA 583
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Thu Mar 9 09:22:24 2006

us-10-071-645-1.rst

Page 14

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D6
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Search completed: March 9, 2006, 05:10:03
Job time : 3955.25 secs


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Db 1080 AAAAAA 1087

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RESULT 3
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; Sequence 10663, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Ducierto, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent .pm
; SEQ ID NO 10663
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 465
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 471
; OTHER INFORMATION: n=a, g, c or t
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; LOCATION: 475
; OTHER INFORMATION: r=a or g
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; NAME/KEY: misc_feature
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; NAME/KEY: misc_feature
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; NAME/KEY: misc_feature
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; LOCATION: 510
; OTHER INFORMATION: k=g or t
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Best Local Similarity 97.8%; Pred. No. 1.7e-82;
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QY 1063 CACACACACACACACACACGAAAAA 1103
Db 444 CACACACACACACACACACGAAAAA 484

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RESULT 4
US-09-702-705-475/c
; Sequence 475, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Panger, Gary
; APPLICANT: Vedrick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Manning, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702.705
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 475
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(417)
; OTHER INFORMATION: n = A,T,C or G
; US-09-702-705-475
Query Match 24.5%; Score 270; DB 3; Length 417;
Best Local Similarity 83.4%; Pred. No. 1e-48;
Matches 342; Conservative 0; Mismatches 62; Indels 6; Gaps 3;
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Qy	695	TGAGAGTGTGGCATCTCTGCTGATTTGGCTGTGTCGCCAATGTTACATATTAATCTTG	754
Db	230	TGAGAGTGTGGCATCTCTGCTGATTTGGCTGTGTCGCCAATGTTACATATTAATCTTG	171
Qy	755	CAAAAATGCTGTGCACTGTGATGTGAATGCAATGCTGTGATTTATTTTATATGTG	814
Db	170	CAAAAATGCTGTGCACTGTGATGTGAATGCTGTGCAATTTATTTTATATATGTG	111
Qy	815	TTATCTCTGATGTACAAAATTTCAAAAATGATCTGTGATATCTGTATATTTT	874
Db	110	TTATCTCTGATGTACAAAATTTCAAAAATGATCTGTGATATCTGTATATTTT	51
Qy	875	GGTCATCTTTAGAACTTATCGAGATGTGTATTAACAGAAAGAACTT	924
Db	50	GGTCATCTTTAGAACTTATCGAGATGTGTATTAACAGAAAGAACTT 1	

```

RESULT 5
US-09-736-457-475/c
: Sequence 475, Application US/09736457
: Patent No. 6509448
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Lodes, Michael A.
: APPLICANT: Fanger, Gary
: APPLICANT: Vedvick, Tom
: APPLICANT: Carter, Darriek
: APPLICANT: Retter, Marc
: APPLICANT: Mennon, Jane
: APPLICANT: Pan, Liqun
: APPLICANT: Wang, Ajun
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121-478C15
: CURRENT APPLICATION NUMBER: US/09/736,457
: CURRENT FILING DATE: 2000-12-13
: NUMBER OF SEQ. ID NOS: 1864
: SOFTWARE: PatSeq0 for Windows Version 3.0
: SEQ ID NO 475
: LENGTH: 417
: TYPE: DNA
: ORGANISM: Homo sapien
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(417)
: OTHER INFORMATION: n = A,T,C or G
US-09-736-457-475

```

	Query March	24.5%; Score 270; DB 3; Length 417;
	Best Local Similarity	83.4%; Pred. No. 1e-48;
Matches	342; Conservative	0; Mismatches 62; Indels 6; Gaps 3
QY	521 ACACAAATATAAATTAATAATTAATCCATATTCATATTAAGAT	580
DB	410 ATATATATTAATTATTAATATATATATCATCTATATNCATATAAAGAAATATAAAG	351
QY	581 AAAAGAGTCTCAGTGCAGATATGGCAATTAATTCATTCTTTTAATACGG-----A	636
DB	350 AAGTCTCAGTGCGACTATTTGTCAAATTAATATCAATTTCTTTTATATATACGTAAT	291
QY	637 ATAATGGCATTAATGAATCTGGATTTTG-AACAATTAATGAAGCGGACC-CGAGTGTTT	694

Db	290	ATTGCCAATTATTAAGATCTGGATTTTGAACAACCTAATATGAACGGCAACACGAGGTTT	23
Qy	695	TGAGGTGTGGCATTCCTCGCTGATTTTGCGTGTCCCAAGTTTCATTTAATTAATCTTG	75
Db	230	TGAGGTGTGGCATTCCTCGCTGATTTTGCGTGTCCCAAGTTTCATTTAATTAATCTTG	17
Qy	755	CAAAATGCTTCTGCGACCTGGATGTGAATAAGTGTGCAGTTTATTTTATTTTATGTTG	81
Db	170	CAAAATGCTTCTGCGACCTGGATGTGAATAAGTGTGCAGTTTATTTTATTTTATGTTG	11
Qy	815	TTATCCTTGATGTACAAAAAATTCAGAAAAATGATCTCTGTAGATATTCCTGTTAATTTT	87
Db	110	TTATCCTTGATGTACAAAAAATTCAGAAAAATGATCTCTGTAGATATTCCTGTTAATTTT	51
Qy	875	GGCATCTTTAGAGTTATCAGGAATGAGTTTAAAAACAAGAGAGACTT	924
Db	50	GGCATCTTTAGAGTTATCAGGAATGAGTTTAAAAACAAGAGAGACTT	1

```

RESULT 6
US-09-614-124B-475/C
Sequence 475, Application US/09614124B
Patent No. 6630574
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Badgur, Chaltanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Panger, Gary
APPLICANT: Veddyck, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.47869
CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 1668
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 475
LENGTH: 417
TYPE: DNA
ORGANISM: Homo sapien
FEATURES:
NAME/KEY: misc_feature
LOCATION: (1)...(417)
OTHER INFORMATION: n = A,T,C or G
US-09-614-124B-475

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Query Match	24.5%;	Score 270;	DB 3;	Length 417;
Best Local Similarity	83.4%;	Pred. No. 1e-48;		
Matches 342;	Conservative 0;	Mismatches 62;	Indels 6;	Gaps 3
QY	521	ACAAATTAATAAAAAAAAAATTTAAATAATAATAAATCCATATCCATATTAAGAT	580	
DB	410	ATPATATAATTTTAAAAATATAATAATTCACATATATACATATAAGAAATAAAAAG	351	
QY	581	AAAAAGTCACAGCGCGATTTGGCAAAATTAATCATTTCTTTTAAATCGGG-----A	636	
DB	350	AGTCGACGTGCAGCGATTTGTCAAAATTAATATCATTTCTTTTAAATACGGTGAAT	291	
QY	637	ATATTCGATTATATAGATCTGGAATTTTG-ACACATATATGAGCGGCAACC-CGAGGTGT	694	
DB	290	ATTGGCAATTTATAGATCTGGAATTTTGAACCACTTAATAGAACGGCAACACAGGTGTTT	231	
QY	695	TAAGGTTCATTCATCTTCGCGATTTTGCGCTGCCAATGTTTACATTAATTAATGTTG	754	
DB	230	TGAGGTTCATTCATCTTCGCGATTTTGCGCTGCCAATGTTTACATTAATTAATCTTG	171	
QY	755	CAAAAATGCTCTGTGCACTTGGATGTGAATGCTGTCCAGCTTAATTTTAAATGTTG	814	
DB	170	CAAAAATGCTCTGTGCACTTGGATGTGAATGCTGTCCAGCTTAATTTTAAATGTTG	111	

Oy	815	TTCACCTGGAGTACAAAAATCAGAAAATGATCTCGTAGATTCGTATTATTT	874
Dd	110	TTCACCTGGAGTACAAAAATTCGAAATGATCTCGTAGATTCGTATTATTT	51
Oy	875	GGCATCTTTGAAGTATATAGAGATGGTTTAAACAAGAAGAACTT	924
Dd	50	GGCATCTTTGAAGATTATACGAATGGTTTTAAACAAGAAGAACTT	1
 RESULT 7 US-09-671-325-475/c Sequence 475, Application US/09671325 Patent No. 6667154 GENERAL INFORMATION: APPLICANT: Mang, Tonglong APPLICANT: Bangur, Chafanya S. APPLICANT: Lodes, Michael A. APPLICANT: Fanger, Gary APPLICANT: Vedvick, Tom APPLICANT: Carter, Darlick APPLICANT: Retter, Marc APPLICANT: Mannion, Jane APPLICANT: Fan, Liqun TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OR INVENTION: DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121-478C12 CURRENT APPLICATION NUMBER: US/09/671,325 CURRENT FILING DATE: 2000-09-26 NUMBER OF SEQ ID NOS: 1825 SOFTWARE: Faets50 for Windows Version 3.0 SEQ ID NO 475 LENGTH: 417 TYPE: DNA ORGANISM: Homo sapien FEATURE: NAME/KEY: misc_feature LOCATION: (1)...(417) OTHER INFORMATION: n = A,T,C or G US-09-671-325-475			
 Query Match 24.5%; Score 270; DB 3; Length 417; Best Local Similarity 83.4%; Pred. No. le=48; Matches 342; Conservative 0; Mismatches 62; Indels 6; Gaps 3			
Oy	521	ACCAATTAATTAATAAAAAAAAAAATTAATAATTAATAATCCATATCCATATTAAGAT	580
Dd	410	ATTAATTAATTAATTAATAATAATAATAATAATTCACATATATCATAATTAAGAATAATAAG	351
Oy	561	AAAAGACTCAGTGCAGTATGGCAAATTAATTAATCAATTTCTTTTAATACGG---A	636
Dd	350	AAGCTCACCTTGACAGCTATTTGTCAAATTAATTAATCAATTTCTTTTAATACGGTGAAT	291
Oy	637	ATAATGGCAATTAATATCTGATTTTGG-AACCATTATAGAACGGCACC-CGAGGTGTTT	694
Dd	230	ATTGCCCAATTTATAGATCTGATTTTGAACACCATTAATAGACGGCAACACGAGTGTTT	231
Oy	695	TGAAGTGTGGCAATCTTCCTGCTATTTGGGTGTTCACATGTTTACATTTTAATCTTG	754
Dd	230	TGAAGTGTGGCAATCTTCCTGCTATTTGGGTGTTCACATGTTTAAATTAATCTTG	171
Oy	755	CAAAATAGTGTGCGACATGGAATGAATAATGCTGCAGTTTATTTTTTTATATGTTG	814
Dd	170	CAAAATAGTGTGCGACTTGGACCTTGAATGGAATGCTGCAGTTTATTTTTTTATATGTTG	111
Oy	815	TTATCCTTGAGATGACAAAAATTCAGAAATGATCTCGTAGATTCGTATTATTT	874
Dd	110	TTATCCTTGAGATGACAAAAATTCAGAAATGATCTCGTAGATTCGTATTATTT	51
Oy	875	GGCATCTTTAAGATTATCAGGAATGGTTTAAACAAGAAGAACTT	924
Dd	50	GGCATCTTTAAGATTATCAGGAATGGTTTAAACAAGAAGAACTT	1

```

RESULT 9
; Sequence 475, Application US/09589184
; Patent No. 6686447
GENERAL INFORMATION:
APPLICANT: Mang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedick, Tom
APPLICANT: Carter, Darlick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C8
CURRENT APPLICATION NUMBER: US/09/589,184
CURRENT FILING DATE: 2000-06-05
NUMBER OF SEQ ID NOS: 827
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 475
LENGTH: 417
TYPE: DNA
ORGANISM: Homo sapien
FEATURES:
NAME/KEY: misc_feature
LOCATION: (1)...(417)
OTHER INFORMATION: n = A,T,C or G
US-09-589-184-475

Query Match      24.5%; Score 270; DB 3; Length 417;
Best Local Similarity 83.4%; Pred. No. 1e-48;
Matches 342; Conservative 0; Mismatches 62; Indels 6; Gaps 3

Qy      521 ACAATTAATAAAAAAAAAAATTAAATATAATAAACCTATATCCATTAAGAT 580
Db      410 ATAAATTAATTTTAAAAATATATAAAATTCACATATATNCATATAAGAAATAAAAG 351

Qy      581 AAAAGATCGACGTGACGATTTGGCAAAATTAATCATCTTTTAAATACGG----A 636
Db      350 AAGTCGATGCAGCTATTGTGCCAAATTAATATCATCTTTTAAATACGGTGAT 291

Qy      637 ATATTGCATTATAGAATCTGGAATTTTG--ACCCTTAATGAAGGGCAC--CGAGGTGTT 694
Db      290 ATTGGCAATTATAGATCTGATTTTAAACACTTAATGAAGGGCACACCGAGTGT 231

Qy      695 TGAGGTGGCGACTTCTTGCGTGAATTTGGCTGTGTCCTCAATGTTACTATTTAATCTTG 754
Db      230 TGAGGTGTGGCAATCTTGCGTGAATTTGGCTGTGTCCTCAATGTTACTATTTAATCTTG 171

Qy      755 CAAAAATGCTTCGTGCACTTGAGTGAATGCTGTCGAGTTTATTTTTTTTATGTG 814
Db      170 CAAAAATGCTTCGTGCACTTGAGTGAATGCTGTCGAGTTTATTTTTTTTATGTG 111

Qy      815 TTATCTTGAGATGACAAAAAATTCAGAAAAATGATCTGTAGATATCTGTGTTATTT 874
Db      110 TTATCTTGAGATGACAAAAAATTCAGAAAAATGATCTGTAGATATCTGTGTTATTT 51

Qy      875 GGTCATCTTAGAAGTTATCGAAGATGTGTTTAAAAACAAGAAAGAACTT 924
Db      50 GGTCATCTTAGAAGTTATCGAAGATGTGTTTAAAAACAAGAAAGAACTT 1

RESULT 9
; Sequence 475, Application US/09658824
; Patent No. 6746846
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
```

```

1 APPLICANT: Vedvick, Tom
2 APPLICANT: Carter, Davidk
3 APPLICANT: Recter, Marc
4 APPLICANT: Mannion, Jame
5 APPLICANT: Fan, Liqun
6 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
7 TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
8 CURRENT PRIORITY DATA: 0121.4578CIS/09/558, 824
9 CURRENT PILING DATE: 2008-09-08
10 NUMBER OF SEQ ID NOS: 1788
11 SOFTWARE: ParseSeq for Windows Version 3.0
12 SEQ ID NO: 475
13 LENGTH: 417
14 TYPE: DNA
15 ORGANISM: Homo sapien
16 FEATURE:
17 NAME/KEY: misc_feature
18 LOCATION: (1)..(417)
19 OTHER INFORMATION: n = A,T,C or G
20 JS-09-658-824-475

```

Query Match	24.5%;	Score 270;	DB 3;	Length 417;
Best Local Similarity	83.4%;	Pred. No. 1e-48;		
Matches 342; Conservative	0;	Mismatches 62;	Indels 6;	Gaps 3

[illegible]

RESULT 10
 US-10-017-754-475/c
 Sequence 475, Application US/10017754
 Patent No. 6858204
 GENERAL INFORMATION:
 APPLICANT: Henderson, Robert A.
 APPLICANT: Wang, Tonglong
 APPLICANT: Watanabe, Yoshihiro
 APPLICANT: Johnson, Jeffrey C.
 APPLICANT: Retter, Marc W.
 APPLICANT: Mamerakis, Margarita
 APPLICANT: Carter, Darryl
 APPLICANT: Fanger, Gary R.
 APPLICANT: Vedrick, Thomas S.
 APPLICANT: Bangur, Chaitanya S.
 APPLICANT: McNabb, Andria
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 OF LUNG CANCER AND DIAGNOSIS OF LUNG CANCER

```

? FILE REFERENCE: 210121.478018
? CURRENT APPLICATION NUMBER: US/10/017,755
? CURRENT FILING DATE: 2001-10-29
? NUMBER OF SEQ ID NOS: 2004
? SOFTWARE: FastSeq for Windows Version 4.0.0
? SEQ ID NO 475
? LENGTH: 417
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURES:
? NAME/KEY: misc_feature
? LOCATION: 370..372
? OTHER INFORMATION: n = A,T,C or G
? US-10-017-954-475

```

Query Match	24.5%	Score 270;	DB 3;	Length 417;
Best Local Similarity	83.4%	Pred. No. 1e-48;		
Matches 342;	Conservative	0;	Mismatches 62;	Indels 6;
			Gaps 3;	

Qy	521	ACAAATPAATATAAAAAATTTAAATATTAATTAATTCCTAATACCTATTAAGAT	58
Db	410	ATAAATPAATATTTAAATATTAATTAATTAATTCATATATNCAATTAAGAAATAAAAAG	35
Qy	581	AAAAAGTCTCAGTGCAGTATTTGGCAAAATTAATTCATTTCTTTTAAATCGGG-----A	63
Db	350	AAGCTCAGTTCCAGCTATTTGTCAAAATTAATTAATTCATTTCTTTTAAATACGGTAAT	29
Qy	637	ATATTCGCAATTAAGATCTGGAATTTTG--ACACCTAATTAAGAGGGACCC--CAAGTGTT	69
Db	290	ATTGGCAGATTAATGATCTGGAATTTTGAACCACTTAATGAAGGGCAACACAGGTGTT	23
Qy	695	TGAGGTGGGCAATCTTGCGCTGATTTGGCTGTCCCAAGTTTACATTAATTAACCTG	75
Db	230	TGAGGTGGGCAATCTTGCGCTGATTTGGCTGTCCCAAGTTTACATTAATTAACCTG	17
Qy	755	CAAAATATGTTCTGTGCATCTGGAATGTGAATAGCTGTCCAGTTATTTTTTTAATGTG	81
Db	170	CAAAATATGTTCTGTGCATCTGGAATGTGAATAGCTGTCCAGTTATTTTTTTAATGTG	11
Qy	815	TTATCTCTGGAATGTACAAAATTAATTCAGAAAATGATCTCTGTGATTAATCTGTTAATTT	87
Db	110	TTATCTCTGGAATGTACAAAATTAATTCAGAAAATGATCTCTGTGATTAATCTGTTAATTT	51
Qy	875	GGTCATCTTTAGAGGTTATCAGGAATGTGTTAAACAGAGAGACTT	924
Db	50	GGTCATCTTTAGAGGTTATCAGGAATGTGTTAAACAGAGAGACTT	1

```

RESULT 11
US-09-651-563-475/c
Sequence 475, Application US/09651563
Patent No. 6914132
GENERAL INFORMATION:
APPLICANT: Mang, Tongrong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodges, Michael A.
APPLICANT: Ranger, Gary
APPLICANT: Vedavick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mainston, Dale
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.478C10 OF LUNG CANCER
CURRENT APPLICATION NUMBER: US/09/651,563
CURRENT FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 1679
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 475
LENGTH: 417
TYPE: DNA
ORGANISM: Homo sapien

```


QY 818 TCCTTGATG 827
DB 327 TCCTTGATG 336

RESULT 14
US-09-513-999C-10536
Sequence 10536, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Giorzano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 10536
LENGTH: 183
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-10536

Query Match 14.1%; Score 155.8; DB 3; Length 183;
Best Local Similarity 97.8%; Pred. No. 2.7e-24;
Matches 179; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 183 AACCACTTTCTGGCGCGGAGCAAGCCGCGCCCAAGCTGGGCGCAATGCGCGG 242
DB 1 AACCACTTTCTGGCGCGGAGCAAGCCGCGCCCAAGCTGGGCGCAATGCGCGG 60
QY 243 AGCAACGGGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 302
DB 61 AGCAACGGGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 303 AAGGCACTTCTGGGCTTGAATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 121 AAGGCACTTCTGGGCTTGAATGATGATGATGATGATGATGATGATGATGATGAT 180
QY 361 GGC 363
DB 181 GGC 183

RESULT 15
US-09-313-300-9
Sequence 9, Application US/09313300
Patent No. 6222027
GENERAL INFORMATION:
APPLICANT: Kaiser Matthew, R.
APPLICANT: Lal, Preeti
APPLICANT: Yue, Henry
APPLICANT: Tang, Tom Y.
APPLICANT: Baughn, Karish, R.
APPLICANT: Azimzal, Yalda
TITLE OF INVENTION: MOLECULES EXPRESSED IN HIPPOCAMPUS
FILE REFERENCE: PR-0012 US
CURRENT APPLICATION NUMBER: US/09/313,300
CURRENT FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PERL Program
SEQ ID NO 9
LENGTH: 1045
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: unsure

LOCATION: (871)...(899)
OTHER INFORMATION: a or g or c or t, unknown, or other
FEATURE:
NAME/KEY:
OTHER INFORMATION: 700122146
PUBLICATION INFORMATION:
US-09-313-300-9

Query Match 10.7%; Score 118.6; DB 3; Length 1045;
Best Local Similarity 62.1%; Pred. No. 4.6e-16;
Matches 259; Conservative 0; Mismatches 144; Indels 14; Gaps 4;

QY 532 AAAAAAAAAAATTTAAATTAATAAATCCCTATATCCCATATTAAGATTAAGAGCTTC 591
DB 2 AATAAATTAATAAATTAATAAATTAATAAATTAATAAATTAATAAATTAATAAAT 61
QY 592 AGTGCATTTGGCAAAATTAATCCATTTCTTTTAAATGCGGAATAT-TGGCATTT 649
DB 62 AGTGCATTTGGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 121
QY 650 AGATCTGATTTTG-ACCACTTAATGAAGCGGCAAGCGGATTTGAGGTGGCAT 708
DB 122 AGATCTGATTTTGACCACTTCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 181
QY 709 TCTTGGCTGATTTGGCTGTTCCCAATGTTTACATTAATTAATCTTGCAAAATGTTCTG 768
DB 182 TCTTGGCTGATTTGGCTGTTCCCAATGTTTACATTAATTAATCTTGCAAAATGTTCTG 241
QY 769 TGGCTGATTTGGAATGCTGTCAG-----TTTTATTTTATGTTTATCTT 822
DB 242 TGGCTGATTTGGAATGCTGTCAG-----TTTTATTTTATGTTTATCTT 301
QY 823 GATGATCAAAATTAATGAATGATGATGATGATGATGATGATGATGATGATGAT 882
DB 302 TTTTGAATGATCAAAATTAATGAATGATGATGATGATGATGATGATGATGATGAT 934
QY 883 TTTTGAATGATCAAAATTAATGAATGATGATGATGATGATGATGATGATGATGAT 934
DB 362 TTTTGAATGATCAAAATTAATGAATGATGATGATGATGATGATGATGATGATGAT 418

Search completed: March 8, 2006, 20:35:11
Job time : 340.112 secs


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QY 757 AAAATGTTCTGTGCACTTGAGATGTAATGCTGTGCACTTTATTTTATGTTT 816
Db 1058 AAAATGTTCTGTGCACTTGAGATGTAATGCTGTGCACTTTATTTTATGTTT 1117
QY 817 ATCTTGATGTAACAAAATTCGAAATGATCTCTGTAGATATCTGTTTATTTTGG 876
Db 1118 ATCTTGATGTAACAAAATTCGAAATGATCTCTGTAGATATCTGTTTATTTTGG 1177
QY 877 TCATCTTGAAGATGATCAGATGATGTTTAAACAGAGAGAACTTTCTAAGGAATG 936
Db 1178 TCATCTTGAAGATGATCAGATGATGTTTAAACAGAGAGAACTTTCTAAGGAATG 1237
QY 937 ATACATGAGAAAGATTTTATTTTAAATGATGTTTAAAGCTGTTGTTTCTGTTGCTGC 996
Db 1238 ATACATGAGAAAGATTTTATTTTAAATGATGTTTAAAGCTGTTGTTTCTGTTGCTGC 1297
QY 997 AAGCTATCTGCCCCAGTTTATGCAATGACACATTTTATGTCAGAAAACACACACA 1056
Db 1298 AAGCTATCTGCCCCAGTTTATGCAATGACACATTTTATGTCAGAAAACACACACA 1357
QY 1057 CACACACACACACACACACACAGAAAAAATTTTATTTTATTTTATTTTATTTT 1104
Db 1358 CACACACACACACACACACACAGAAAAAATTTTATTTTATTTTATTTTATTTT 1405

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RESULT 3
US-09-820-649-25
; Sequence 25, Application US/09820649
; Publication No. US2003019683A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 83 Human Secreted Proteins
; FILE REFERENCE: P2012P1
; CURRENT APPLICATION NUMBER: US/09/820,649
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US/09/236,557
; PRIOR FILING DATE: 1999-01-26
; PRIOR APPLICATION NUMBER: PCT/US98/15949
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: 60/054,212
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,209
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,234
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,218
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,214
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,236
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,215
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,211
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 353
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 1510
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (39)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-820-649-25

```

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Query Match 63.4% Score 699.8; DB 3; Length 1510;
Best Local Similarity 89.7%; Pred. No. 2,4e-155;
Matches 893; Conservative 1; Mismatches 69; Indels 33; Gaps 12;

```

```

QY 141 GCCAGCTGGGCGAGATCTTCTCTGCGGCTGACAGACACCAACTTCTTGCGCC 200
Db 2 GCCAGCTGGGCGAGATCTTCTCTGCGGCTGACAGACACCAACTTCTTGCGCC 61
QY 201 GGGGAGAAACAGCGGCGCCCGCCAGCTGGGCGAGATGCGCCGAGCAAGCGGGTGTATT 260
Db 62 GGGGAGAAACAGCGGCGCG-CCAGCTGGGCGAGATGCGCCGAGCAAGCGGGTGTATT 120
QY 261 GAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 319
Db 121 GAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
QY 320 TAACT-CCCCAAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 378
Db 181 TAACTCCCCAAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 240
QY 379 CAAGAAAGATGAAAGAGAGAGACCTTGAAATTTATTTATTTATTTATTTATTTATTT 437
Db 241 CAAGAAAGATGAAAGAGAGAGACCTTGAAATTTATTTATTTATTTATTTATTTATTT 300
QY 438 AATGACAACTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCT 495
Db 301 AATGACAACTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCTGTATCT 360
QY 496 GAGAGAAAGAGGCTTGCGC-CTCTGACAAATTAATTAATTAATTAATTAATTAATTA 554
Db 361 GAGAGAAAGAGGCTTGCGCCTCTGACAAATTAATTAATTAATTAATTAATTAATTA 420
QY 555 AAAATCCCTTA------TCCATTAATTAATTAATTAATTAATTAATTAATTAATTA 594
Db 421 AAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
QY 595 GCAGATATGCGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 650
Db 481 GCATTTTGTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 540
QY 651 GATCTGATTTTG-ACCACTTAATGAGCGGC-ACCOCAGGTTTGAAGTGTGCGCAT 708
Db 541 GATCTGATTTTGAACCACTTAATGAGCGGCACACAGGTTTGAAGTGTGCGCAT 600
QY 709 TCTTGGTGATTTGGTGTTGCCAATGTTTACATTAATTAATTAATTAATTAATTAATTA 768
Db 601 TCTTGGTGATTTGGTGTTGCCAATGTTTACATTAATTAATTAATTAATTAATTAATTA 660
QY 768 TGCACTGGAATGGAAGAGCGTGCAGTTTATTTTATTTATTTATTTATTTATTTATTTAT 828
Db 661 TGCACTGGAATGGAAGAGCGTGCAGTTTATTTTATTTATTTATTTATTTATTTATTTAT 720
QY 828 ACAAATAATTCAGAAATGATCTGTAGATTTCTGTTTATTTTATTTTATTTTATTTATTT 888
Db 721 ACAAATAATTCAGAAATGATCTGTAGATTTCTGTTTATTTTATTTTATTTTATTTATTT 780
QY 888 GTTATCAGAGATGTTTAAACAGAGAGAACTTTCTAAGAAATGATATACAGAAA 948
Db 781 GTTATCAGAGATGTTTAAACAGAGAGAACTTTCTAAGAAATGATATACAGAAA 840
QY 948 GATTTTATTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1008
Db 841 GATTTTATTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
QY 1009 CAAGTATGCAAAATGACACATTTTATGTCAGAAAACACACACACACACACACACAC 1068
Db 901 CAAGTATGCAAAATGACACATTTTATGTCAGAAAACACACACACACACACACACAC 960
QY 1069 CACACACACACACACACACACACACACACACACACACACACACACACACACACAC 1104
Db 961 CACACACACACACACACACACACACACACACACACACACACACACACACACACAC 996

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RESULT 4
US-10-160-162-25
; Sequence 25, Application US/10160162
; Publication No. US2003016654A1

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Qy	237	GGCGGAGCAAGCGGTTGTTATGAAATATATGAGTTATGACGTCGCTGAAAAATATG	236
Db	1813	GGCGGAGCAAGCGGTTGTTATGAAATATATGAGTTATGACGTCGCTGAAAAATATG	175
Qy	297	ACCGAACAAGCAACT - CTGGTGCTTACT - CCCCAAGCAATAGTTAAGGAAAGAT	354
Db	1753	ACCGAACAAGCAACTCTCGGTGCTTACTCCCCAAGCAATAGTTAAGGAAAGAT	169
Qy	355	AGGAACCGCGGTAACTATTGCGAAAAGCATGAAAAGAAAAGCATCTTGAATTTA	414
Db	1653	AGGAACCGCGGTAAAGTATTGCGAAAAGCATGAAAAGAAAAGCATCTTGAATTTA	163
Qy	415	TTTACTGCTTG - TACCGAGATGAATCAACACTGTATCTGGTAT - ATGCCGGAAC	472
Db	1633	TTTACTGCTTGCTACCGAGATGAATCAACACTGTATCTGGTATCAAGCCGGAAC	157
Qy	473	AGATTAGGCGA - AGAGAAAGAGAGAGAAAGAAAGCTTGGGC - CCTCTCAAAATAAA	530
Db	1573	AGATTAGGCGAAGAGAGAGAGAGAGAGAAAGCTCTGGGCTCCTCTCAAAATAAA	151
Qy	531	TAATAAAAAAAAAATTTAAATATATAAAATCCCTATA - -----TCCATAT	574
Db	1513	AAATATAAAAAAAAAATTTAAATATATAAAATTCATATATACATATAAG	145
Qy	575	AAAGATTAAGAAGCTCAGT --- GCAGTATGCGAAATTAATCAATCTTTTAT	630
Db	1453	AAATATAAAAAAAAAAGTCTGAGTCACTATTTGCAAAATATATCAATCTTTTATA	139
Qy	631	ACGGAAATTT --- GGCATTATAGATCGAATTTTG - ACGATTATGAAGGGC - ACC	684
Db	1393	TACGGGAATATGCGCAATTATATCTGCAATTTTGAAACCTTATATGAAGCGCA	133
Qy	685	CGAGGCTTTGAAGGTATGGCAATCTCGGTATTTGGCTGTCCAAATGTTACATA	744
Db	1333	CGAGGCTTTGAAGGTATGGCAATCTCGGTATTTGGCTGTCCAAATGTTACATA	127
Qy	745	TTTATCTTGCAAAATGCTTCTGCACTTGGATGAAATGCTGTCAGTTAATTT	804
Db	1273	TTTATCTTGCAAAATGCTTCTGCACTTGGATGAAATGCTGTCAGTTAATTT	121
Qy	805	TTTTATGTTGTTACTCTGGATGTACAAAATTCAGAAAATGATCTCTGATATATCT	864
Db	1213	TTTTATGTTGTTACTCTGGATGTACAAAATTCAGAAAATGATCTCTGATATATCT	115
Qy	865	GTTTATTTTGGTCACTTTAGAAAGTATCGAAAGTGTTTAAACAAGAGAAACTT	924
Db	1153	GTTTATTTTGGTCACTTTAGAAAGTATCGAAAGTGTTTAAACAAGAGAAACTT	109
Qy	925	TTCTAAGAAATATCAATTAAGAAATTTTATTTTAAATGAGTGTAAAGCTGTGTT	984
Db	1093	TTCTAAGAAATATCAATTAAGAAATTTTATTTTAAATGAGTGTAAAGCTGTGTT	103
Qy	985	CTTTGTTGCTGAAGCTATCTGCCAATGTAAAGCAATTTTATATGCA	104
Db	1033	CTTTGTTGCTGAAGCTATCTGCCAATGTAAAGCAATTTTATATGCA	974
Qy	1045	AAAAACACACACACACACACACACACACACACACGAAAAA	110
Db	973	AAAAACACACACACACACACACACACACACACACGAAAAA	914

RESULT 7
US-10-198-846-11350
Sequence 11350, Application US/10198846
Publication No. US2003009974A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER

```

1 FILE REFERENCE: MRI-049
2 CURRENT APPLICATION NUMBER: US/10/198,846
3 CURRENT FILING DATE: 2002-07-18
4 PRIOR APPLICATION NUMBER: 60/306,220
5 PRIOR FILING DATE: 2001-07-18
6 NUMBER OF SEQ. ID NOS.: 14084
7 SOFTWARE: FastSeq for Windows Version 4.0
8 SEQ. ID NO. 11350
9 LENGTH: 1850
10 TYPE: DNA
11 ORGANISM: Homo sapiens
12 PRACTICE:
13 NAME/KEY: misc_feature
14 LOCATION: 1..26,107..1839,1940,1841,1842,1843,1844,1845,1846,
15 LOCATION: 1847,1848,1849,1850
16 OTHER INFORMATION: n = A,T,C or G
17 US-10-198-846-11350

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Query Match 57.5%; Score 634.6; DB 5; Length 1850;

Matches	833;	Conservative	0;	Mismatches	94;	Indels	32;	Gaps	11;
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[illegible]

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Qy 925 TTCTAAGGAATGATCAGTAAAGATTTTATTTAAATGAGTGTGAAGCTGTGCTT 984
Db 972 TTTTACAGGATGATACATGAGAAAGATTTTATTTAAATGAGTGTGAAGCTGTGCTT 1031
Qy 985 CTTTGTGCTGCAAGCTATCTGCCAAGTAAATGACATCTTTTATGTGCA 1044
Db 1032 CTTTGTGCTGCAAGCTATCTGCCAAGTAAATGACATCTTTTATGTGCA 1091
Qy 1045 AAAACACACACACACACACACACACACACACACACACACACACACACACACAC 1103
Db 1092 AAAACACACACACACACACACACACACACACACACACACACACACACACACAC 1150

RESULT 8
US-10-172-118-1796
; Sequence 1796, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-17599
; CURRENT APPLICATION NUMBER: US/10/172,118
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1796
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_018584
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1796

Query Match 57.3%; Score 632.6; DB 6; Length 1321;
Best Local Similarity 89.0%; Pred. No. 26-139;
Matches 816; Conservative 0; Mismatches 69; Indels 32; Gaps 11;
```

```
Db 361 TATATACATATATTAAGAAATTAAGAAAGCTCAGCTGACGATTTTGCAAATAT 420
Qy 614 ATCCATTTCTTTTAAATACGGG---AATTTGGCATTTATGATCTGGATTTTG ACCAC 668
Db 421 ATCCATTTCTTTTAAATACGGGATATATGATCTGGATTTATGATCTGGATTTTG 480
Qy 669 TTAATGAAGCGGC-ACCCAGGTGTTTGGAGTGTGCAATCTTGCTGATTTGGCTGT 727
Db 481 TTAATGAAGCGGCACACACAGGTGTTTGGAGTGTGCAATCTTGCTGATTTGGCTGT 540
Qy 728 TCCCAATGTTTACATTTTATATCTTGCAAAAATGTTTCTGTGACCTTGATGTGAATG 787
Db 541 TCCCAATGTTTACATTTTATATCTTGCAAAAATGTTTCTGTGACCTTGATGTGAATG 600
Qy 788 CTGTCAAGTTTATTTTATTTTATGTTTATCTTGATGATGATACAAAATTCAGAAAATG 847
Db 601 CTGTCAAGTTTATTTTATTTTATGTTTATCTTGATGATGATGATACAAAATTCAGAAAATG 660
Qy 848 ATCTGTGATATTTCTGTTTATTTTATGTCATCTTTGAGAGTATACAGGAATGTGTTA 907
Db 661 ATCTGTGATATTTCTGTTTATTTTATGTCATCTTTGAGAGTATACAGGAATGTGTTA 720
Qy 908 AAAACAGAGAGAACTTTCTTAAAGATGATACATGAAAGATTTTATTTAAATGAG 967
Db 721 AAAACAGAGAGAACTTTCTTAAAGATGATACATGAAAGATTTTATTTAAATGAG 780
Qy 968 TTTTAAAGCTTTGTTTCTTTGTTGCTGCAAGCTATCTGCCAAGTAAATGCAATGAC 1027
Db 781 TTTTAAAGCTTTGTTTCTTTGTTGCTGCAAGCTATCTGCCAAGTAAATGCAATGAC 840
Qy 1028 ACATTTTATTTTATGTCAGAAAACACACACACACACACACACACACACACACACACAC 1087
Db 841 ACATTTTATTTTATGTCAGAAAACACACACACACACACACACACACACACACACACAC 900
Qy 1088 AAAAAAAAAAAAAAAAAA 1104
Db 901 ACGAAAAACAAAGAAAA 917

RESULT 9
US-10-342-887-1796
; Sequence 1796, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1796
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1796

Query Match 57.3%; Score 632.6; DB 7; Length 1321;
Best Local Similarity 89.0%; Pred. No. 26-139;
Matches 816; Conservative 0; Mismatches 69; Indels 32; Gaps 11;
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QY 220 CCAAGCTGGCCAGATCGCCGCGAGCAAGCGGGTGTATTAGATGATGATGATGATG 279
DB 1 CCAAGCTGGCCAGATCGCCGCGAGCAAGCGGGTGTATTAGATGATGATGATGATG 60
QY 280 ACGTCTGAAAAATATGACCAAGGACACT-CTGTGTCTAACT-CCCCAAGCAAT 337
DB 61 ACGTCTGAAAAATATGACCAAGGACACTCTGTGTCTAACTCCCCAAGCAAT 120
QY 338 GAGTTAAGGAGAGATAGAAACGGCGGTAAAGTTATGGCAAAAAGCATGAAAAGAGA 397
DB 121 GAGTTAAGGAGAGATAGAAACGGCGGTAAAGTTATGGCAAAAAGCATGAAAAGAGA 180
QY 398 AAGCATTTGAAATTTATCTAGCTTG-TACCAAGATGAAATCAACACTGTATCTG 456
DB 181 AAGCATTTGAAATTTATCTAGCTTGCTCTACCAAGATGAAATCAACACTGTATCTG 240
QY 457 GTAT-ATGCCCGAGACAGATTAGCCGA-AGAGAGAAAGAGAGAAAGAGAGCTTGGG 514
DB 241 GTATCAGGCCCGAGACAGATTAGCCGAAGAGAGAGAGAGAGAGAGAGCTTGGG 300
QY 515 C-CTCTCAAAATATATATATATATATATATATATATATATATATATATATATAT 566
DB 301 CTCTCTGCAAAAATATATATATATATATATATATATATATATATATATATATATAT 360
QY 567 -----TCCCATATAGATATATATATATATATATATATATATATATATATATAT 613
DB 361 TATATACATATATATATATATATATATATATATATATATATATATATATATATAT 420
QY 614 ATCCATTTCTTTTATATATATATATATATATATATATATATATATATATATATAT 668
DB 421 ATCCATTTCTTTTATATATATATATATATATATATATATATATATATATATATAT 480
QY 669 TTAATAGAGCGGC-ACCCAGAGTGTGTTGAGGTGTGGCAATTCCTGCTGATTTGG 727
DB 481 TTAATAGAGCGGCACACAGAGTGTGTTGAGGTGTGGCAATTCCTGCTGATTTGG 540
QY 728 TCCCATATGTTTATATATATATATATATATATATATATATATATATATATATAT 787
DB 541 TCCCATATGTTTATATATATATATATATATATATATATATATATATATATATAT 600
QY 788 CTGTCCAGTTATATATATATATATATATATATATATATATATATATATATATAT 847
DB 601 CTGTCCAGTTATATATATATATATATATATATATATATATATATATATATATAT 660
QY 848 ATCTGTGATATATCTGTGTTATATATATATATATATATATATATATATATATAT 907
DB 661 ATCTGTGATATATCTGTGTTATATATATATATATATATATATATATATATATAT 720
QY 908 AAACAGAGAGAGACCTTTCTAAGAGATATATATATATATATATATATATATATAT 967
DB 721 AAACAGAGAGAGACCTTTCTAAGAGATATATATATATATATATATATATATATAT 780
QY 968 TTGTAAGCTGTGTGTTCTTTGTCGCAAGGTATCTGCCAGTTATATGCAATGAGC 1027
DB 781 TTGTAAGCTGTGTGTTCTTTGTCGCAAGGTATCTGCCAGTTATATGCAATGAGC 840
QY 1028 ACATTTTATATGTCAGAAAACACACACACACACACACACACACACACACACAC 1087
DB 841 ACATTTTATATGTCAGAAAACACACACACACACACACACACACACACACACAC 900
QY 1088 AAAAAAAAAAAAAAAAAA 1104
DB 901 ACGAAAAACAAAGAAA 917
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RESULT 10

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US-10-956-157-2260/c
; Sequence 2260, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
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; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2260
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-2260

Query Match 57.3%; Score 632.6; DB 9; Length 1321;
Best Local Similarity 89.0%; Pred. No. 2e-139; Indels 32; Gaps 11;
Matches 816; Conservative 0; Mismatches 69;

QY 220 CCAAGCTGGCCAGATCGCCGCGAGCAAGCGGGTGTATTAGATGATGATGATGATG 279
DB 1321 CCAAGCTGGCCAGATCGCCGCGAGCAAGCGGGTGTATTAGATGATGATGATGATG 1262
QY 280 ACGTCTGAAAAATATGACCAAGGACACT-CTGTGTCTAACT-CCCCAAGCAAT 337
DB 1261 ACGTCTGAAAAATATGACCAAGGACACTCTGTGTCTAACTCCCCAAGCAAT 1202
QY 338 GAGTTAAGGAGAGATAGAAACGGCGGTAAAGTTATGGCAAAAAGCATGAAAAGAGA 397
DB 1201 GAGTTAAGGAGAGATAGAAACGGCGGTAAAGTTATGGCAAAAAGCATGAAAAGAGA 1142
QY 398 AAGCATTTGAAATTTATCTAGCTTG-TACCAAGATGAAATCAACACTGTATCTG 456
DB 1141 AAGCATTTGAAATTTATCTAGCTTGCTCTACCAAGATGAAATCAACACTGTATCTG 1082
QY 457 GTAT-ATGCCCGAGACAGATTAGCCGA-AGAGAGAAAGAGAGAGAGAGAGAGAGAGCTTGG 514
DB 1081 GTATCAGGCCCGAGACAGATTAGCCGAAGAGAGAGAGAGAGAGAGAGAGAGCTTGG 1022
QY 515 C-CTCTCAAAATATATATATATATATATATATATATATATATATATATATATAT 566
DB 1021 CTCTCTGCAAAAATATATATATATATATATATATATATATATATATATATATATAT 962
QY 567 -----TCCCATATAGATATATATATATATATATATATATATATATATATATAT 613
DB 961 TATATACATATATATATATATATATATATATATATATATATATATATATATATAT 902
QY 614 ATCCATTTCTTTTATATATATATATATATATATATATATATATATATATATATAT 668
DB 901 ATCCATTTCTTTTATATATATATATATATATATATATATATATATATATATATAT 720
QY 669 TTAATAGAGCGGC-ACCCAGAGTGTGTTGAGGTGTGGCAATTCCTGCTGATTTGG 727
DB 721 TTAATAGAGCGGCACACAGAGTGTGTTGAGGTGTGGCAATTCCTGCTGATTTGG 782
QY 728 TCCCATATGTTTATATATATATATATATATATATATATATATATATATATATAT 787
DB 781 TCCCATATGTTTATATATATATATATATATATATATATATATATATATATATAT 722
QY 788 CTGTCCAGTTATATATATATATATATATATATATATATATATATATATATATAT 847
DB 721 CTGTCCAGTTATATATATATATATATATATATATATATATATATATATATATAT 662
QY 848 ATCTGTGATATATCTGTGTTATATATATATATATATATATATATATATATATATAT 907
DB 661 ATCTGTGATATATCTGTGTTATATATATATATATATATATATATATATATATATAT 720
QY 908 AAACAGAGAGAGACCTTTCTAAGAGATATATATATATATATATATATATATATAT 967
DB 601 AAACAGAGAGAGACCTTTCTAAGAGATATATATATATATATATATATATATATAT 780
QY 968 TTGTAAGCTGTGTGTTCTTTGTCGCAAGGTATCTGCCAGTTATATGCAATGAGC 1027
DB 541 TTGTAAGCTGTGTGTTCTTTGTCGCAAGGTATCTGCCAGTTATATGCAATGAGC 482
QY 1028 ACATTTTATATGTCAGAAAACACACACACACACACACACACACACACACACAC 1087
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RESULT 14
US-09-978-360A-155
; Sequence 155, Application US/09978360A
; Publication No. US20040110939A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Mline
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56:US4.CIP
; CURRENT APPLICATION NUMBER: US/09/978.360A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.Dm
; SEQ ID NO 155
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 327..416
; FEATURE:
; NAME/KEY: POLYA Site
; LOCATION: 404..417
US-09-978-360A-155

Query Match          36.7%; Score 405.4; DB 3; Length 417;
Best Local Similarity 98.0%; Pred. No. 9.1e-86;
Matches 409; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 690 TGTTCAGAGTGGTGCATCTTGGCTGATGTTGGCTGTCCTCCATGTTTACATTATTAA 749
DB 1 TGTTCAGAGTGGTGCATCTTGGCTGATGTTGGCTGTCCTCCATGTTTACATTATTAA 60
QY 750 TCTTGCAAAATGCTTCGTGCACTTGATGTAATGCTGTCAGTTTATTTTTTTTAA 809
DB 61 TCTTGCAAAATGCTTCGTGCACTTGATGTAATGCTGTCAGTTTATTTTTTTTAA 120
QY 810 TGTTCATCTTCGTGATGTAACAAAATTCAGAAAATGATCTCTGTAGATAATCTGTTT 869
DB 121 TGTTCATCTTCGTGATGTAACAAAATTCAGAAAATGATCTCTGTAGATAATCTGTTT 180
QY 870 ATTTCGTCACTTTTGAAGATTATCAGGAATGTTGTTTAAACAGAGAGAACCTTTCTA 929
DB 181 ATTTCGTCACTTTTGAAGATTATCAGGAATGTTGTTTAAACAGAGAGAACCTTTCTA 240
QY 930 AGGATGATCATAGAAAGATTTTATTTTAAATGATGTTAAGCTTGTTCTTTG 989
|||||
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DB 241 AGGATGATCATAGAAAGATTTTATTTTAAATGATGTTAAGCTTGTTCTTTG 300
QY 990 TTGCTGCAAGCTATCTGCCCAAGTTAATGCAATGAGACACATTTTATGTCAGAAAAC 1049
DB 301 TTGCTGCAAGCTATCTGCCCAAGTTAATGCAATGAGACACATTTTATGTCAGAAAAC 360
QY 1050 ACACACACACACACACACACACACACACACACACACACACACACACACACACACAC 1104
DB 361 ACACACACACACACACACACACACACACACACACACACACACACACACACACACAC 415

RESULT 15
US-10-027-632-231746
; Sequence 231746, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Mang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-32
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231746
; LENGTH: 584
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(584)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-231746

Query Match          34.5%; Score 380.4; DB 5; Length 584;
Best Local Similarity 98.0%; Pred. No. 9.5e-80;
Matches 384; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 713 CGCTGATTTGGCTGCTCCCAAGTTTACATTATTATCTTGCAAAAATGCTTCGTGCA 772
DB 1 CGCTGATTTGGCTGCTCCCAAGTTTACATTATTATCTTGCAAAAATGCTTCGTGCA 60
QY 773 CTTCGATGTAATGCTGTCAGTTTATTTTTTTTATGTTGTTATCTTCGATGTAACAA 832
DB 61 CTTCGATGTAATGCTGTCAGTTTATTTTTTTTATGTTGTTATCTTCGATGTAACAA 120
QY 833 AAAATTCAGAAAATGATCTCTGTAGATAATCTGTTTATTTTGGTCATCTTTAGAACTTA 892
DB 121 AAAATTCAGAAAATGATCTCTGTAGATAATCTGTTTATTTTGGTCATCTTTAGAACTTA 180
QY 893 TCAGGAATGCTTTTAAACAGAGAGAACCTTTCTAAGGAATGATATAGAAAGATT 952
DB 181 TCAGGAATGCTTTTAAACAGAGAGAACCTTTCTAAGGAATGATATAGAAAGATT 240
QY 953 TTAATTTAAATGATGTTAAGCTTGTTGTTCTTTGTTGCTGCAAGCTATCTGCCAAG 1012
DB 241 TTAATTTAAATGATGTTAAGCTTGTTGTTCTTTGTTGCTGCAAGCTATCTGCCAAG 300
QY 1013 TTAATGCAAAATGACACATTTTATGTCAGAAAACACACACACACACACACACAC 1072
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Thu Mar 9 09:22:23 2006

us-10-071-645-1.rnpbm

Page 12

D_b 301 TTTATGCGAATTGACACTTTTTCATGTGCAGAAAAACACACACACACACACACA 360
Q_y 1073 CACACACACACGAAAAAAAAAAAAAAAAAAAA 1104
D_b 361 CACACACACACACACGAAAAAACCTAAAGAAA 392

Search completed: March 8, 2006, 23:09:47
Job time : 783.432 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 22:09:41 ; Search time 343.055 Seconds
(without alignments)
7425.207 Million cell updates/sec

Title: US-10-071-645-1

Perfect score: 1104
Sequence: 1 ggcacgagcgagcgccgctg.....aaaaaaaaaaaaaaaa 1104

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 7673375 seqs, 115364844 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.New.*

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2: /cgn2_6/prodata/2/pubna/US06_NEW_PUB.seq.*
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6: /cgn2_6/prodata/2/pubna/US10_NEW_PUB.seq1.*
7: /cgn2_6/prodata/2/pubna/US10_NEW_PUB.seq1.*
8: /cgn2_6/prodata/2/pubna/US10_NEW_PUB.seq1.*
9: /cgn2_6/prodata/2/pubna/US11_NEW_PUB.seq2.*
10: /cgn2_6/prodata/2/pubna/US11_NEW_PUB.seq3.*
11: /cgn2_6/prodata/2/pubna/US11_NEW_PUB.seq3.*
12: /cgn2_6/prodata/2/pubna/US11_NEW_PUB.seq4.*
13: /cgn2_6/prodata/2/pubna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	405.4	36.7	417	5	US-09-978-360A-155 Sequence 155, App
2	60	5.4	545	6	US-09-925-065A-530238 Sequence 530238, A
3	59.6	5.4	600	6	US-09-925-065A-467081 Sequence 467081, A
4	57.6	5.2	577	6	US-09-925-065A-233526 Sequence 233526, A
5	57.6	5.2	577	6	US-09-925-065A-233527 Sequence 233527, A
6	57.2	5.2	525	6	US-09-925-065A-593182 Sequence 593182, A
7	57.2	5.2	525	6	US-09-925-065A-593183 Sequence 593183, A
8	57.2	5.2	562	6	US-09-925-065A-366163 Sequence 366163, A
9	57.2	5.2	600	12	US-11-136-527-7013 Sequence 7013, App
10	57.2	5.2	4712	12	US-11-136-527-2917 Sequence 2917, App
11	36.4	5.1	201	8	US-10-995-561-30380 Sequence 30380, A
12	36.4	5.1	201	8	US-10-995-561-30380 Sequence 30380, A
13	36.4	5.1	1483	6	US-09-925-065A-693654 Sequence 693654, A
14	36.4	5.1	1483	6	US-09-925-065A-693655 Sequence 693655, A
15	56.4	5.1	187786	8	US-10-995-561-13474 Sequence 13474, A
16	56	5.1	650	6	US-09-925-065A-891461 Sequence 891461, A
17	56	5.1	650	6	US-09-925-065A-914488 Sequence 914488, A
18	55.6	5.0	187986	8	US-10-995-561-13252 Sequence 13252, A
19	55.6	5.0	201	8	US-10-995-561-30368 Sequence 30368, A
20	55.6	5.0	201	8	US-10-995-561-30371 Sequence 30371, A

21	55.6	5.0	201	8	US-10-995-561-30374 Sequence 30374, A
22	55.6	5.0	650	6	US-09-925-065A-891462 Sequence 891462, A
23	55.6	5.0	650	6	US-09-925-065A-891463 Sequence 891463, A
24	55.4	5.0	3406	6	US-09-925-065A-83767 Sequence 83767, A
25	55.4	5.0	3406	6	US-09-925-065A-83767 Sequence 83767, A
26	55.2	5.0	201	8	US-10-995-561-30377 Sequence 30377, A
27	55	5.0	545	6	US-09-925-065A-834433 Sequence 834433, A
28	55	5.0	562	6	US-09-925-065A-279475 Sequence 279475, A
29	54.8	5.0	782	7	US-10-349-331-728 Sequence 728, App
30	54.6	4.9	569	6	US-09-925-065A-603624 Sequence 603624, App
31	54.6	4.9	574	7	US-10-349-331-821 Sequence 821, App
32	54.4	4.9	1739	6	US-09-925-065A-709966 Sequence 709966, App
33	54.2	4.9	551	6	US-09-925-065A-328525 Sequence 328525, App
34	54.2	4.9	90572	12	US-11-124-358A-2900 Sequence 2900, App
35	54.2	4.9	330183	7	US-10-330-772-937 Sequence 301129, App
36	54	4.9	385	6	US-09-925-065A-301129 Sequence 301130, App
37	54	4.9	585	6	US-09-925-065A-189360 Sequence 189360, App
38	54	4.9	607	6	US-09-925-065A-189360 Sequence 189360, App
39	54	4.9	615	6	US-09-925-065A-877775 Sequence 877775, App
40	54	4.9	205388	7	US-10-330-772-537 Sequence 537, App
41	53.8	4.9	550	6	US-09-925-065A-647106 Sequence 647106, App
42	53.8	4.9	550	6	US-09-925-065A-647108 Sequence 647108, App
43	53.8	4.9	550	6	US-09-925-065A-647109 Sequence 647109, App
44	53.8	4.9	1127	6	US-09-925-065A-23780 Sequence 23780, A
45	53.8	4.9	1127	6	US-09-925-065A-26953 Sequence 26953, A

ALIGNMENTS

RESULT 1
US-09-978-360A-155
Sequence 155, Application US/09978360A
Publication No. US2006009633a9
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste Dumas Milne
APPLICANT: Duclert, Aymeric
APPLICANT: Bouguetere, Lydie
APPLICANT: Jobert, Severin
APPLICANT: Cluse, Catherine
FILE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
TITLE REFERENCE: 56, US4, CIP
CURRENT APPLICATION NUMBER: US/09/978, 360A
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/066, 677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/069, 957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: US 60/074, 121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: US 60/081, 563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: US 60/096, 116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 60/099, 273
PRIOR FILING DATE: -09-04
PRIOR APPLICATION NUMBER: US 09/191, 997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: US 09/215, 435
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: PCT/IB98/02122
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: US 09/247, 155
PRIOR FILING DATE: 1999-02-09
Remaining prior application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 810
SOFTWARE: Patent .pm
SEQ ID NO 155
LENGTH: 417
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS

LOCATION: 327..416
FEATURE:
NAME/KEY: polyA site
LOCATION: 404..417
US-09-978-360A-155

Query Match 36.7%; Score 405.4; DB 5; Length 417;
Best Local Similarity 98.6%; Pred. No. 5,1e-55;
Matches 409; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 690 TGTTCAGGTGTTGGCATTCTTCCCTGATTTGGCTCCCAAGTTTACATTATTAA 749
DB 1 TGTTCAGGTGTTGGCATTCTTCCCTGATTTGGCTCCCAAGTTTACATTATTAA 60
QY 750 TGTTCAGAAAATGTTCTGTGCACTTGGATGTAATGCTGCTGCTTTATTTTAA 809
DB 61 TGTTCAGAAAATGTTCTGTGCACTTGGATGTAATGCTGCTGCTTTATTTTAA 120
QY 810 TGTTCATTCCTTGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 869
DB 121 TGTTCATTCCTTGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 180
QY 870 ATTTTGTGATCTTTAGAAATTTACGAATGTTTAAACAGAGAACTTTTCTA 929
DB 181 ATTTTGTGATCTTTAGAAATTTACGAATGTTTAAACAGAGAACTTTTCTA 240
QY 930 AGGAATGATACATGAAAGATTTTAAATGATGTAAGCTTGTGTTCTTGG 989
DB 241 AGGAATGATACATGAAAGATTTTAAATGATGTAAGCTTGTGTTCTTGG 300
QY 990 TTCTGCAAGCTATCTGCCCAAGTTATGCAATGACACATTTTATGTCAGAAAAC 1049
DB 301 TTCTGCAAGCTATCTGCCCAAGTTATGCAATGACACATTTTATGTCAGAAAAC 360
QY 1050 AC 1104
DB 361 AC 415

RESULT 2
US-09-925-065A-530238
Sequence 530238, Application US/09925065A
Publication No. US20040181048A1

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 530238
LENGTH: 545
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-530238

Query Match 5.4%; Score 60; DB 6; Length 545;
Best Local Similarity 65.3%; Pred. No. 0.85;
Matches 87; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
972 AAAGCTGTGTCTTCTTGTGCTGCAAGCTATCTGCCCAAGTTAATGCAATGACACAT 1031

DB 361 AATGCATGTGATTTTAACTTGCACAGAGACTTTGATTTGCTTACTCAATATATCTTCT 420
QY 1032 TTTTATGTCAGAAAAC 1091
DB 421 CCCTTCCTTCTGAAACACACACACACACACACACACACACACACACACACACAA 480
QY 1092 AAAAAAAAAA 1103
DB 481 CAAAAAAAAA 492

RESULT 3
US-09-925-065A-467081

Sequence 467081, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 467081
LENGTH: 600
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-467081

Query Match 5.4%; Score 59.6; DB 6; Length 600;
Best Local Similarity 58.4%; Pred. No. 0.99;
Matches 104; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 927 CTAGGAATGATACATGAAAGATTTTAAATGAGTTGTAAGCTTGTGTTCT 986
DB 160 CTAGGAATGATACATGAAAGATTTTAAATGAGTTGTAAGCTTGTGTTCT 219
QY 987 TTGTGCTGCAAGCTATCTGCTGCAAGTTATGCAATGACACATTTTATGTCAGAA 1046
DB 220 TTGTGCTGCAAGCTATCTGCTGCAAGTTATGCAATGACACATTTTATGTCAGAA 279
QY 1047 AAC 1104
DB 280 CAC 337

RESULT 4
US-09-925-065A-233526/c

Sequence 233526, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20

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1 PRIOR APPLICATION NUMBER: US 60/250,092
2 PRIOR FILING DATE: 2000-11-30
3 PRIOR APPLICATION NUMBER: US 60/261,766
4 PRIOR FILING DATE: 2001-01-16
5 PRIOR APPLICATION NUMBER: US 60/289,846
6 PRIOR FILING DATE: 2001-05-09
7 NUMBER OP SRO ID NOS: 957086
8 SOFTWARE: PAGESEQ for Windows Version 4.0
9 SRO ID NO 233526
10 LENGTH: 577
11 TYPE: DNA
12 ORGANISM: Homo sapiens
13 US-09-925-065A-233526

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```

Query Match      5.2%; Score 57.6; DB 6; Length 577;
Best Local Similarity 93.8%; Pred. No. 2;
Matches 60; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy      1041 CAGAAAAACACACACACACACACACACACACACACACACGAAAAAAAAAAAAAAAA 1100
Db      485 CACACACACACACACACACACACACACACACACACACACACACAAAAAAAA 426

Oy      1101 AAAA 1104
Db      425 AAAA 422

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```

RESULT 5
US-09-925-065A-233527/c
? Sequence 233527, Application US/09925065A
? Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925_065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/743_096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/752,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/750,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/761,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/789,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: ParseSeq for Windows Version 4.0
SEQ ID NO 233527
LENGTH: 577
TYPE: DNA
? ORGANISM: Homo sapiens
US-09-925-065A-233527

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[illegible]

RESULT 6
US-09-925-065A-593182
; Sequence 593182, Application US/09925065A
; Publication No. US2004018104A1

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1  GENERAL INFORMATION:
2  APPLICANT: Wang, David G.
3  TITLE OF INVENTION: Identification and Mapping of Single
4  Nucleotide Polymorphisms in the Human Genome
5  FILE REFERENCE: 108827.135
6  CURRENT APPLICATION NUMBER: US/09/925,065A
7  CURRENT FILING DATE: 2001-08-08
8  PRIOR APPLICATION NUMBER: US 60/243,096
9  PRIOR FILING DATE: 2000-10-24
10 PRIOR APPLICATION NUMBER: US 60/252,147
11 PRIOR FILING DATE: 2000-11-20
12 PRIOR APPLICATION NUMBER: US 60/250,092
13 PRIOR FILING DATE: 2000-11-30
14 PRIOR APPLICATION NUMBER: US 60/261,746
15 PRIOR FILING DATE: 2001-01-16
16 PRIOR APPLICATION NUMBER: US 60/289,846
17 PRIOR FILING DATE: 2001-05-09
18 NUMBER OF SEQ ID NOS: 957086
19 SOFTWARE: FastSeq for Windows Version 4.0
20 SEQ ID NO 593182
21 LENGTH: 525
22 TYPE: DNA
23 ORGANISM: Homo sapiens
24 US-09-925-065A-593182

```

[illegible]

```

RESULT 7
US-09-925-065A-593183
Sequence 593183, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT FILING DATE: 2001-08-08
PRIORITY APPLICATION NUMBER: US/09/925, 065A
PRIORITY FILING DATE: 2001-08-08
PRIORITY APPLICATION NUMBER: US 60/243, 096
PRIORITY FILING DATE: 2000-10-24
PRIORITY APPLICATION NUMBER: US 60/252, 147
PRIORITY FILING DATE: 2000-11-20
PRIORITY APPLICATION NUMBER: US 60/250, 092
PRIORITY FILING DATE: 2000-11-30
PRIORITY APPLICATION NUMBER: US 60/261, 766
PRIORITY FILING DATE: 2001-01-16
PRIORITY APPLICATION NUMBER: US 60/289, 846
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PARASEQ FOR WINDOWS Version 4.0
SEQ ID NO 593183
LENGTH: 525
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-593183

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Query Match          5.2%; Score 57.2; DB 6; Length 525;
Best Local Similarity .72.5%; Pred. No. 2.3;
Matches 74; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
07 1003 TCTGCCCGACAGTAAATGCAATGTCACATTTTATGTCCAGAAAAACACACACACACA 1062
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

Db 398 TCAGCCCACTGCAACGAGTGAATATAAAAAGCTTTATGTCTCACACACACACACACA 457

Qy 1063 CACACACACACACACACACACGAAAAAAAAAAAAAAAAAAAA 1104

458 CACACACACACACACACGCAAAAAAAAAAAAAAAAAAAAA 499

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RESULT 8
US-09-925-065A-366163
; Sequence 366163, Application US/09925065A
; Publication No. US2004018048A1
; GENERAL INFORMATION:
; Applicant: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243.096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252.147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250.092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261.766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289.846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 366163
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-366163

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[illegible]

```

RESULT 9
US-11-136-527-7013
; Sequence 7013, Application US/1136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-04100 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7013
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-7013

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Query Match	5.2%;	Score 57.2;	DB 12;	Length 600;
Best Local Similarity	45.3%;	Pred. No. 2.4;		
Matches 77; Conservative	30;	Mismatches 63;	Indels 0;	Gaps 0;

QY 935 TGAATACATAGAAAAAGATTTTATTTTAAATAAGTGTGAACGTCGTGTTCTGTCST 994
 195 KKTWTWTTTAAATTAATKTKWAAATTTTAAATTTTCTKKTGTGTGWTGTTGG 254
 Db 995 GCAAGCTATCTGCCAAGTTAATGCATAATGACATCTTTTATGTAGAGAAAACACCA 1054
 QY 995 GAGGAGTAAAGTTCTTTAGCACAAATGTTTACATATTTGTACCAAAAAAATTWCAC 314
 Db 255 CAC 1104
 QY 1055 CAC 1104
 Db 315 CAC 364

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RESULT 10
US-11-136-527-2917
; Sequence 2917, Application US/1136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2917
; LENGTH: 4712
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2917

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RESULT 11
US-10-995-561-30380
; Sequence 30380. Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: C1001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ. ID NOS: 65702
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ. ID NO 30380
LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-30380

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Query Match 5.1%; Score 56.4; DB 8; Length 201;


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Best Local Similarity 72.0%; Pred. No. 2.8;
Matches 72; Conservative 1; Mismatches 27; Indels 0; Gaps 0;

Qy 1004 CTGCCAAGTTAATGCAATGTCATTTTATGTCAGAAAAACACACACACAC 1063
Db 23 CTGACCTCCAGCCTGCTGGGTGACAGATCCATACACACACATTCACACACAC 82
Qy 1064 ACACACACACACACACACACACACACACACACACACACACACACACAC 1103
Db 83 ACACACACACACACACACACACACACACACACACACACACACACACACAC 122

RESULT 12
US-10-995-561-77752
; Sequence 77752, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: C0001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 77752
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-77752

Query Match 5.1%; Score 56.4; DB 8; Length 201;
Best Local Similarity 72.0%; Pred. No. 2.8;
Matches 72; Conservative 1; Mismatches 27; Indels 0; Gaps 0;

Qy 1004 CTGCCAAGTTAATGCAATGTCATTTTATGTCAGAAAAACACACACACAC 1063
Db 23 CTGACCTCCAGCCTGCTGGGTGACAGATCCATACACACACATTCACACACAC 82
Qy 1064 ACACACACACACACACACACACACACACACACACACACACACACACAC 1103
Db 83 ACACACACACACACACACACACACACACACACACACACACACACACACAC 122

RESULT 13
US-09-925-065A-693654
; Sequence 693654, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 693654
; LENGTH: 1483
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-693654

```

```

Query Match 5.1%; Score 56.4; DB 6; Length 1483;
Best Local Similarity 88.2%; Pred. No. 3.5;
Matches 60; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1037 ATGTCAAAAACACACACACACACACACACACACACACACACACACAC 1096
Db 436 AAGAAATATACACACACACACACACACACACACACACACACACACAC 495
Qy 1097 AAAAAAAA 1104
Db 496 AAAAAAAA 503

RESULT 14
US-09-925-065A-693655
; Sequence 693655, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 693655
; LENGTH: 1483
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-693655

Query Match 5.1%; Score 56.4; DB 6; Length 1483;
Best Local Similarity 88.2%; Pred. No. 3.5;
Matches 60; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1037 ATGTCAAAAACACACACACACACACACACACACACACACACACACAC 1096
Db 436 AAGAAATATACACACACACACACACACACACACACACACACACACAC 495
Qy 1097 AAAAAAAA 1104
Db 496 AAAAAAAA 503

RESULT 15
US-10-995-561-13474
; Sequence 13474, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: C0001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 13474
; LENGTH: 187786
; TYPE: DNA

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Thu Mar 9 09:22:24 2006

us-10-071-645-1.rnpbn

Page 6

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
LOCATION: (1) (187786)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13474

Query Match 5.1%; Score 56.4; DB 8; Length 187786;
Best Local Similarity 72.0%; Pred. No. 5.6; Indels 0; Gaps 0;
Matches 72; Conservative 1; Mismatches 27

QY 1004 CTGCCAAGTTAATGCAATGACATTTTATGTCAGAAAAACACACACACACAC 1063
DB 61772 CTGCATCTCCAGCCCTGCGGTGACAGATCTTATCACACACATACACACACAC 61831
QY 1064 AC 1103
DB 61832 AC 61871

Search completed: March 8, 2006, 22:32:43
Job time : 345.055 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus.p2n model

Run on: March 8, 2006, 20:35:31 ; Search time 151 Seconds

(Without alignments)
1000.614 Million cell updates/sec

Title: US-10-071-645-2

Sequence: 453 1 MMEVLPYGBDKLSPYGDCD.....VKNMTDKAPVNSPKTMS 85

Scoring table:

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1303057 segs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seg length: 0

Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-Q=/abs/ABSSWEB/spool/US10071645/runat_08032006_115126_4724/app_query.fasta_1
-DB=Issued_Patents_NA -PMT=fastap -SUFFIX=g2n.rml -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human4.0.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-HOST=abs02p -USER=US10071645 @CGN 1 1 512 @runat_08032006_115126_4724
-NCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Issued Patents NA:

- 1: /cgn2_6/prodata/1/ina/1 COMB.seg:*
- 2: /cgn2_6/prodata/1/ina/5 COMB.seg:*
- 3: /cgn2_6/prodata/1/ina/6A COMB.seg:*
- 4: /cgn2_6/prodata/1/ina/6B COMB.seg:*
- 5: /cgn2_6/prodata/1/ina/H COMB.seg:*
- 6: /cgn2_6/prodata/1/ina/PCUS COMB.seg:*
- 7: /cgn2_6/prodata/1/ina/RE COMB.seg:*
- 8: /cgn2_6/prodata/1/ina/RE COMB.seg:*
- 9: /cgn2_6/prodata/1/ina/Backfile1.seg:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	413	91.2	1581	3	US-09-313-300-1
2	413	91.2	1876	3	US-09-566-921-70
3	241	53.2	183	3	US-09-513-999C-10536
4	111.5	24.6	315	3	US-09-621-976-15158
5	71.5	15.8	447	3	US-09-710-279-3121
6	71.5	15.8	654	3	US-09-134-001C-2356
7	71.5	15.8	4218	3	US-09-710-279-4205
8	68.5	15.1	426	3	US-10-012-819-31
9	68.5	15.1	471	3	US-10-012-819-241

10	68	15.0	336	2	US-08-081-539-88	Sequence 88, Appl
11	68	15.0	336	2	US-08-466-647-88	Sequence 88, Appl
12	67.5	14.9	15885	3	US-09-949-016-11927	Sequence 11927, A
13	67.5	14.9	15885	3	US-09-949-016-15627	Sequence 15627, A
14	67	14.8	342	2	US-08-081-539-78	Sequence 78, Appl
15	67	14.8	342	2	US-08-466-647-78	Sequence 78, Appl
16	66	14.6	315	2	US-08-081-539-89	Sequence 89, Appl
17	66	14.6	315	2	US-08-466-647-89	Sequence 89, Appl
18	66	14.6	358	3	US-09-624-268B-6	Sequence 6, Appl1
19	66	14.6	381	3	US-09-252-991A-15810	Sequence 15810, A
20	66	14.6	550	3	US-09-115-407-22	Sequence 22, Appl
21	66	14.6	870	3	US-09-252-991A-15882	Sequence 15882, A
22	66	14.6	1317	3	US-09-252-991A-15836	Sequence 15836, A
23	66	14.6	2073	3	US-09-252-991A-15779	Sequence 15779, A
24	65.5	14.5	4403765	3	US-09-103-840A-2	Sequence 1, Appl1
25	65.5	14.5	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
26	65	14.3	906	2	US-07-797-553-1	Sequence 1, Appl1
27	65	14.3	912	2	US-07-797-553-3	Sequence 3, Appl1
28	65	14.3	2880	3	US-09-614-221A-485	Sequence 485, App
29	64.5	14.2	747	3	US-09-252-991A-2924	Sequence 2924, Ap
30	64.5	14.2	1362	3	US-09-252-991A-2945	Sequence 2945, Ap
31	64.5	14.2	1551	3	US-09-252-991A-13034	Sequence 13034, Ap
32	64.5	14.2	61198	3	US-09-949-016-17248	Sequence 17248, A
33	64	14.1	2734	9	5104637-26	Parent No. 5104637
34	64	14.1	3575	3	US-09-023-655-1395	Sequence 1395, Ap
35	63.5	14.0	601	3	US-09-948-016-16963	Sequence 16963, A
36	63.5	14.0	601	3	US-09-948-016-16964	Sequence 16964, A
37	63.5	14.0	657	3	US-09-252-991A-10023	Sequence 10023, A
38	63.5	14.0	99748	3	US-09-252-991A-9632	Sequence 9632, Ap
39	63.5	14.0	99748	3	US-09-949-016-11590	Sequence 11590, A
40	63.5	14.0	99749	3	US-09-949-016-16518	Sequence 16518, A
41	63	13.9	330	2	US-08-081-539-84	Sequence 84, Appl
42	63	13.9	330	2	US-08-466-647-84	Sequence 84, Appl
43	63	13.9	333	2	US-08-411-795B-114	Sequence 114, App
44	63	13.9	333	2	US-08-411-795B-115	Sequence 115, App
45	63	13.9	333	2	US-08-469-319A-114	Sequence 114, App

ALIGNMENTS

RESULT 1
US-09-313-300-1
/ Sequence 1, Application US/09313300
/ Patent No. 6222027
/ GENERAL INFORMATION:
/ APPLICANT: Kaser, Matthew, R.
/ APPLICANT: Lal, Preeti
/ APPLICANT: Lal, Preeti
/ APPLICANT: Tang, Tom Y.
/ APPLICANT: Baughn, Mariah, R.
/ APPLICANT: Rajmala, Valda
/ TITLE OF INVENTION: MOLECULES EXPRESSED IN HIPPOCAMPUS
/ FILE REFERENCE: FB-0012 US
/ CURRENT APPLICATION NUMBER: US/09/313,300
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PERL Program
/ SEQ ID NO 1
/ LENGTH: 1581
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: OTHER INFORMATION: 239240
/ PUBLICATION INFORMATION:
/ US-09-313-300-1
Alignment Scores:
Pred. No.: 1.99e-50
Score: 413.00
Percent Similarity: 96.6%
Best Local Similarity: 96.6%
Query Match: 91.2%
Length: 1581
Matches: 84
Conservative: 0
Mismatch: 1
Indels: 2

DB: 3 Gaps: 0

US-10-071-645-2 (1-85) x US-09-313-300-1 (1-1581)

QY 1 MetTrpGluValLeuProTyrGlyAspGluValLeuSerProTyrGlyAspGlyValAsp 20

DB 39 ATGCGAGAGGTCTGCTCCACGCGACGAGACCTAGCCCTACGCGACGCGCGCGAC 98

QY 21 ValGlyGlnIlePheSerCysArgLeuGlyAspThrAsnAsnPhenPheGlyValIleGlyGln 40

DB 99 GTGGGCGCAATCTCTCTCCGCTGCGACGACCACTTCTTCCGCGCGCGCGACG 158

QY 41 AsnLysArgProProLysLeuGlyGlnIleGlyArgSerLysArgValIleGlyAsp 60

DB 159 AACCAAGCG 218

QY 61 AspArgIleAspAspValLeuLysAsnMetThrAspLysAlaPro-IleuValSerAsn 80

DB 219 GATAGGATTGATGACGCTGTAATAATGACGACGACGACCTCTGATGCTTACTC 278

QY 80 r-ProlyThrMetSer 85

DB 279 CCCCAAGACAAATGACT 295

RESULT 2

US-09-566-921-70

/ Sequence 70, Application US/09566921

/ Patent No. 6682888

/ GENERAL INFORMATION:

/ APPLICANT: Loring, Jeanne F.

/ APPLICANT: Tingley, Debora W.

/ APPLICANT: Edwards, Carla M.

/ TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE

/ FILE REFERENCE: PA-0024 US

/ CURRENT APPLICATION NUMBER: US/09/566,921

/ CURRENT FILING DATE: 2000-05-05

/ NUMBER OF SEQ ID NOS: 138

/ SOFTWARE: PERL Program

/ SEQ ID NO 70

/ LENGTH: 1876

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ FEATURES:

/ NAME/KEY: misc feature

/ OTHER INFORMATION: Inocyte ID No. 6682888 234151.1

/ NAME/KEY: unsave

/ LOCATION: 1360, 1362-1391, 1864

/ OTHER INFORMATION: a, t, c, g, or other

US-09-566-921-70

Alignment Scores:

Pred. No.: 2 51e-50 Length: 1876

Score: 413.00 Matches: 84

Percent Similarity: 96.6% Conservative: 0

Best Local Similarity: 96.6% Mismatches: 1

Query Match: 91.2% Indels: 2

DB: 3 Gaps: 0

US-10-071-645-2 (1-85) x US-09-566-921-70 (1-1876)

QY 1 MetTrpGluValLeuProTyrGlyAspGluValLeuSerProTyrGlyAspGlyValAsp 20

DB 355 ATGCGAGAGGTCTGCTCCACGCGACGAGACCTAGCCCTACGCGACGCGCGCGAC 414

QY 21 ValGlyGlnIlePheSerCysArgLeuGlyAspThrAsnAsnPhenPheGlyValIleGlyGln 40

DB 415 GTGGGCGCAATCTCTCTCCGCTGCGACGACCACTTCTTCCGCGCGCGCGACG 474

QY 41 AsnLysArgProProLysLeuGlyGlnIleGlyArgSerLysArgValIleGlyAsp 60

DB 475 AACCAAGCG 534

QY 61 AspArgIleAspAspValLeuLysAsnMetThrAspLysAlaPro-IleuValSerAsn 80

DB 535 GATAGGATTGATGACGCTGTAATAATGACGACGACGACCTCTGATGCTTACTC 594

QY 80 r-ProlyThrMetSer 85

DB 595 CCCCAAGACAAATGACT 611

RESULT 3

US-09-513-999C-10536

/ Sequence 10536, Application US/09513999C

/ Patent No. 6783961

/ GENERAL INFORMATION:

/ APPLICANT: Dumas Milne Edwards, J.B.

/ APPLICANT: Duclet, A.

/ APPLICANT: Giordano, J.Y.

/ TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

/ FILE REFERENCE: 59, US2, REG

/ CURRENT APPLICATION NUMBER: US/09/513,999C

/ CURRENT FILING DATE: 2000-02-24

/ PRIOR APPLICATION NUMBER: US 60/122,487

/ PRIOR FILING DATE: 1999-02-26

/ NUMBER OF SEQ ID NOS: 36681

/ SOFTWARE: Patent.pm

/ SEQ ID NO 10536

/ LENGTH: 183

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-09-513-999C-10536

Alignment Scores:

Pred. No.: 1 55e-26 Length: 183

Score: 241.00 Matches: 52

Percent Similarity: 94.5% Conservative: 0

Best Local Similarity: 94.5% Mismatches: 1

Query Match: 53.2% Indels: 2

DB: 3 Gaps: 0

US-10-071-645-2 (1-85) x US-09-513-999C-10536 (1-183)

QY 33 AsnAsnPhenPheGlyValIleGlyAspGluValLeuSerProTyrGlyAspGlyValAsp 52

DB 1 AACCACTTCTTACG 60

QY 53 SerLysArgValIleGlyAspAspArgIleAspAspValLeuLysAsnMetThrAsp 72

DB 61 AGCAACCGGGTGTATTGAAATGATGATGATGATGATGATGATGATGATGATGATG 120

QY 73 LysAlaPro-IleuValSerAsnSer-ProLysThrMetSer 85

DB 121 AAGGACACTCTGCTGCTTAACTCCCAAGACAAATGACT 161

RESULT 4

US-09-621-976-15158

/ Sequence 15158, Application US/09621976

/ Patent No. 6639063

/ GENERAL INFORMATION:

/ APPLICANT: Dumas Milne Edwards, J.B.

/ APPLICANT: Jobert, S.

/ APPLICANT: Giordano, J.Y.

/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.

/ FILE REFERENCE: GENSET, 054PR2

/ CURRENT APPLICATION NUMBER: US/09/621,976

/ CURRENT FILING DATE: 2000-07-21

/ NUMBER OF SEQ ID NOS: 19335

/ SOFTWARE: Patent.pm

/ SEQ ID NO 15158

/ LENGTH: 315

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-09-621-976-15158

Alignment Scores:

Pred. No.: 6.69 Length: 4218
Score: 71.50 Matches: 19
Percent Similarity: 52.5% Conservative: 13
Best Local Similarity: 31.1% Mismatches: 20
Query Match: 15.8% Indels: 9
DB: 3 Gaps: 2

US-10-071-645-2 (1-85) x US-09-710-279-4205 (1-4218)

QY 21 ValGlyInIlePheSerCysArgLeuGlnAspThrAsnAspPheGlyAlaGlyGln 40
DB 3103 ATGGGTAAATTAACGATGCTCATGTTAGAGATTAAATAC-----GCTATTAGA 3153
QY 41 AsnLysArgProFrolyLeuGlyGlnIleGlyArgSerLysArgValValIleGluAsp 60
DB 3154 AATTAAGATTACCACTGATA-----AAAGAGTCATTGAGAGAGAT 3195
QY 61 AspArgIleAspAspValLeuLysAsnMetThrAspLysAlaProLeuValSerAsnSer 80
DB 3196 GAAGATATTGATGATTATACGTTAACTGTCATACAGATTACTTAATTGATTATGAC 3255
QY 81 Pro 81
DB 3256 CCA 3258

RESULT 8

US-10-012-819-31
Sequence 31, Application US/10012819
Patent No. 6916615

GENERAL INFORMATION:
APPLICANT: Legrain, Pierre
APPLICANT: Sella, Luc
APPLICANT: Rain, Jean-Christophe
TITLE OF INVENTION: Collection of Prokaryotic DNA for Two-Hybrid System, Helicobacter
FILE REFERENCE: B5053
CURRENT APPLICATION NUMBER: US/10/012,819
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: BP 99401066.8
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 426
TYPE: DNA
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(426)
US-10-012-819-31

Alignment Scores:

Pred. No.: 0.826 Length: 426
Score: 68.50 Matches: 20
Percent Similarity: 40.7% Conservative: 15
Best Local Similarity: 23.3% Mismatches: 28
Query Match: 15.1% Indels: 23
DB: 3 Gaps: 3

US-10-071-645-2 (1-85) x US-10-012-819-31 (1-426)

QY 7 TyrGlyAspGluLysLeuSerProTyrGlyAspGlyValGlyAspValGlyInIlePheSer 26
DB 175 TATGGCAGCAAGACTTGAGTCTTT----- 201
QY 27 CysArgLeuGlnAspThrAsnAspPheGlyAlaGlyGlnAsnLysArgProFroly 46
DB 202 -----GCCAATTAATTTTGTGCTGAGGCTTGATCAAGCCCTTGATTA 246
QY 47 LeuGlyGlnIleGlyArgSerLysArgVal-----ValIleGluAspAspArgIleAsp 64
DB 247 ATAGGCTCTAGCTCTGATGCAAGACTTACAGAACTTCTTGATTAAGACACTTTTGGG 306

QY 65 AspValLeuLysAsnMetThrAspLysAlaProLeuValSerAsn----- 79
DB 307 GATATTTAATCAATGATTGACAGAGCCCTTATCAATTAATCAATCTATTCTTGCTG 366
QY 80 SerProlyThrMetSer 85
DB 367 GGTCCGACAGATTGAC 384

RESULT 9

US-10-012-819-241
Sequence 241, Application US/10012819
Patent No. 6916615

GENERAL INFORMATION:
APPLICANT: Legrain, Pierre
APPLICANT: Sella, Luc
APPLICANT: Rain, Jean-Christophe
TITLE OF INVENTION: Collection of Prokaryotic DNA for Two-Hybrid System, Helicobacter
FILE REFERENCE: B5053
CURRENT APPLICATION NUMBER: US/10/012,819
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: BP 99401066.8
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 241
LENGTH: 471
TYPE: DNA
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(471)
US-10-012-819-241

Alignment Scores:
Pred. No.: 0.947 Length: 471
Score: 68.50 Matches: 20
Percent Similarity: 40.7% Conservative: 15
Best Local Similarity: 23.3% Mismatches: 28
Query Match: 15.1% Indels: 23
DB: 3 Gaps: 3

US-10-071-645-2 (1-85) x US-10-012-819-241 (1-471)

QY 7 TyrGlyAspGluLysLeuSerProTyrGlyAspGlyValGlyAspValGlyInIlePheSer 26
DB 1 TATGGCAGCAAGACTTGAGTCTTT----- 27
QY 27 CysArgLeuGlnAspThrAsnAspPheGlyAlaGlyGlnAsnLysArgProFroly 46
DB 28 -----GCCAATTAATTTTGTGCTGAGGCTTGATCAAGCCCTTGATTA 72
QY 47 LeuGlyGlnIleGlyArgSerLysArgVal-----ValIleGluAspAspArgIleAsp 64
DB 73 ATAGGCTCTAGCTCTGATGCAAGACTTACAGAACTTCTTGATTAAGACACTTTTGGG 132
QY 65 AspValLeuLysAsnMetThrAspLysAlaProLeuValSerAsn----- 79
DB 133 GATATTTAATCAATGATTGACAGAGCCCTTATCAATTAATCAATCTATTCTTGCTG 192
QY 80 SerProlyThrMetSer 85
DB 193 GGTCCGACAGATTGAC 210

RESULT 10

US-08-081-539-88
Sequence 88, Application US/08081539
Patent No. 5501962

GENERAL INFORMATION:
APPLICANT: Bradford-Goldberg, Sarah R.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.

APPLICANT: Olin, Peter O.
TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine
TITLE OF INVENTION: Chimeric Hybrid Polypeptides
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate
ADDRESSEE: Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081,539
FILING DATE: 19930621
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kanady, Mary J.
REGISTRATION NUMBER: 28623
REFERENCE/DOCKET NUMBER: 2724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6881
TELEFAX: (708)470-6501
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-081-539-88
Alignment Scores:
Pred. No.: 0.709 Length: 336
Score: 68.00 Matches: 20
Percent Similarity: 44.1% Conservative: 6
Best Local Similarity: 33.9% Mismatches: 27
Query Match: 15.0% Indels: 6
DB: 2 Gaps: 1
US-10-071-645-2 (1-85) x US-08-081-539-88 (1-336)
QY 29 LeuGlnAspThrAsnAspPheGlyAlaGlyGln-----AsnLys 42
DB 61 CTGCTGACCTTCAACACCTCAATGTCGAAGCAAGATATCTCGATGAAATAAATTAACCTT 120
QY 43 ArgProProlLysLeuGlnIleGlyArgSerLysArgValValIleGlnAspArg 62
DB 121 CCGCTCCAAACCTTCAGGACATTCACCGTTCACGAGGTGAAGTGACATGATCAGCA 180
QY 63 IleAspAspValLeuLysAsnMetThrAspLysAlaProLeuValSerAsnSerPro 81
DB 181 ATTGAAGCATTTCTTAAATAATCTCTGCCATGTCGCCCCCTGGCCACGCGCCGACCC 237
RESULT 11
US-08-466-647-88
Sequence 88, Application US/08466647
Patent No. 5543141
GENERAL INFORMATION:
APPLICANT: Bratford-Goldberg, Sarah R.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Olin, Peter O.
TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine
TITLE OF INVENTION: Chimeric Hybrid Polypeptides
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:

ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate
ADDRESSEE: Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,647
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,539
FILING DATE: 21-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kanady, Mary J.
REGISTRATION NUMBER: 28623
REFERENCE/DOCKET NUMBER: 2724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6881
TELEFAX: (708)470-6501
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-466-647-88
Alignment Scores:
Pred. No.: 0.709 Length: 336
Score: 68.00 Matches: 20
Percent Similarity: 44.1% Conservative: 6
Best Local Similarity: 33.9% Mismatches: 27
Query Match: 15.0% Indels: 6
DB: 2 Gaps: 1
US-10-071-645-2 (1-85) x US-08-466-647-88 (1-336)
QY 29 LeuGlnAspThrAsnAspPheGlyAlaGlyGln-----AsnLys 42
DB 61 CTGCTGACCTTCAACACCTCAATGTCGAAGCAAGATATCTCGATGAAATAAATTAACCTT 120
QY 43 ArgProProlLysLeuGlnIleGlyArgSerLysArgValValIleGlnAspArg 62
DB 121 CCGCTCCAAACCTTCAGGACATTCACCGTTCACGAGGTGAAGTGACATGATCAGCA 180
QY 63 IleAspAspValLeuLysAsnMetThrAspLysAlaProLeuValSerAsnSerPro 81
DB 181 ATTGAAGCATTTCTTAAATAATCTCTGCCATGTCGCCCCCTGGCCACGCGCCGACCC 237
RESULT 12
US-09-949-016-11927
Sequence 11927, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11927
LENGTH: 15585
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1) .. (15585)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11927

Alignment Scores:
Pred. No.: 151
Score: 67.50
Percent Similarity: 44.4%
Best Local Similarity: 30.2%
Query Match: 14.9%
DB: 3
Length: 15585
Matches: 19
Conservative: 9
Mismatch: 30
Indels: 5
Gaps: 2

US-10-071-645-2 (1-85) x US-09-949-016-11927 (1-15585)

QY 2 TTPGIVAlleupProTyrgIyAspGluYsLeuSer-----ProTyrgIyAsp 17
DB 8530 TGGAGCTCATTTACAAAGGCCAGAAACAGACTCTGGTGGCTGAGACCAGGTGGAGCT 8589
QY 18 GYGIVAspValGlyGlnIlePheSerCyArg---LeuGlnAspThrAsnAsnPhePhe 36
DB 8590 GCGGGGAGCAGTGGGTGTTTCTGAGCTATTAAAGCGAGAGCCAAAGACTTTGGA 8649
QY 37 GYAlaGlyGlnAsnIyAspGlyGlnIleGlyArgSerIyAspVal 56
DB 8650 GCGACTGACATGAGCTGAGAGAAAGGGGAGTTGGGGGCAAGTCCAAAGGCT 8709
QY 57 ValIleGlu 59
DB 8710 CTGGCTGAG 8718

RESULT 13
US-09-949-016-15627
Sequence 15627: Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949, 016
FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15627
LENGTH: 15585
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1) .. (15585)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15627

Alignment Scores:
Pred. No.: 151
Score: 67.50
Percent Similarity: 44.4%
Best Local Similarity: 30.2%
Length: 15585
Matches: 19
Conservative: 9
Mismatch: 30

Query Match: 14.9%
DB: 3
Indels: 5
Gaps: 2

US-10-071-645-2 (1-85) x US-09-949-016-15627 (1-15585)

QY 2 TTPGIVAlleupProTyrgIyAspGluYsLeuSer-----ProTyrgIyAsp 17
DB 8530 TGGAGCTCATTTACAAAGGCCAGAAACAGACTCTGGTGGCTGAGACCAGGTGGAGCT 8589
QY 18 GYGIVAspValGlyGlnIlePheSerCyArg---LeuGlnAspThrAsnAsnPhePhe 36
DB 8590 GCGGGGAGCAGTGGGTGTTTCTGAGCTATTAAAGCGAGAGCCAAAGACTTTGGA 8649
QY 37 GYAlaGlyGlnAsnIyAspGlyGlnIleGlyArgSerIyAspVal 56
DB 8650 GCGACTGACATGAGCTGAGAGAAAGGGGAGTTGGGGGCAAGTCCAAAGGCT 8709
QY 57 ValIleGlu 59
DB 8710 CTGGCTGAG 8718

RESULT 14
US-08-081-539-78
Sequence 78: Application US/08081539
Patent No. 5501952
GENERAL INFORMATION:
APPLICANT: Batford-Goldberg, Sarah R.
APPLICANT: Klein, Barbara K.
APPLICANT: McGear, Judith P.
APPLICANT: Oline, Peter O.
TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine
Chimeric Hybrid Polypeptides
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081,539
FILING DATE: 19930621
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kanady, Mary J.
REGISTRATION NUMBER: 28623
REFERENCE/DOCKET NUMBER: 2724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 470-6501
TELEFAX: (708) 470-6881
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-081-539-78

Alignment Scores:
Pred. No.: 102
Score: 67.00
Percent Similarity: 47.5%
Best Local Similarity: 32.8%
Query Match: 14.8%
Length: 342
Matches: 20
Conservative: 9
Mismatch: 24
Indels: 8

DB: 2 Gaps: 2
US-10-071-645-2 (1-85) x US-08-081-539-78 (1-342)
QY 29 LeuGlnAspThrAsnAspPheGlyAlaGlyGln-----AsnLys 42
DB 61 CTGCTGACTTCACCACTCAATGATGGAAGACCAAGATATCTGATGGAATAATACCTT 120
QY 43 ArgProFroLysLeuGlyGlnIleGlyArgSerLysArgValValIleGluAspAspArg 62
DB 121 CGTGTCCAAACCTCGAGCATTCACCGGTCTGTCAGTCTCTGACGCCGGAAGACCTT 180
QY 63 -----IleAspAspValLeuLysAsnMetThrAspLysAlaProLeuValSerAsnSer 80
DB 181 TACGTTATCGAATCCATCTCTGAAAAACCTGCTCCGCTGACCGCTAGCCAGCGCCGCA 240
QY 81 Pro 81
DB 241 CCC 243
RESULT 15
US-08-466-647-78
; Sequence 78, Application US/0846647
; Patent No. 5543141
; GENERAL INFORMATION:
; APPLICANT: Bradford-Goldberg, Sarah R.
; APPLICANT: Bascon, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olin, Peter O.
; TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine
; TITLE OF INVENTION: Chimeric Hybrid Polypeptides
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,647
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,539
; FILING DATE: 21-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanady, Mary J.
; REGISTRATION NUMBER: 28623
; REFERENCE/DOCKET NUMBER: 2724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708)470-6501
; TELEFAX: (708)470-6881
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-466-647-78
Alignment Scores:
Pred. No.: 1.02 Length: 342
Score: 67.00 Matches: 20
Percent Similarity: 47.5% Conservative: 9

Best Local Similarity: 32.8% Mismatches: 24
Query Match: 14.8% Indels: 8
DB: 2 Gaps: 2
US-10-071-645-2 (1-85) x US-08-466-647-78 (1-342)
QY 29 LeuGlnAspThrAsnAspPheGlyAlaGlyGln-----AsnLys 42
DB 61 CTGCTGACTTCACCACTCAATGATGGAAGACCAAGATATCTGATGGAATAATACCTT 120
QY 43 ArgProFroLysLeuGlyGlnIleGlyArgSerLysArgValValIleGluAspAspArg 62
DB 121 CGTGTCCAAACCTCGAGCATTCACCGGTCTGTCAGTCTCTGACGCCGGAAGACCTT 180
QY 63 -----IleAspAspValLeuLysAsnMetThrAspLysAlaProLeuValSerAsnSer 80
DB 181 TACGTTATCGAATCCATCTCTGAAAAACCTGCTCCGCTGACCGCTAGCCAGCGCCGCA 240
QY 81 Pro 81
DB 241 CCC 243

Search completed: March 8, 2006, 20:59:47
Job time : 161 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: March 8, 2006, 23:49:43 ; Search time 789 Seconds

(without alignments)
890.871 Million cell updates/sec

Title: US-10-071-645-2

Sequence: 1 MWEVLPGDEKLSPYGGCD.....VLKMTDKAPLVNSPKTWS 85

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 9793542 segs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seg length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=published.Applications.NA.Main -QFMT=fastap -SUFFIX=g2n.rnpbm
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-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pcr -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs806p
-USER=US10071645 @CGN 1.1549 @runat_08032006.115128.4779 -NCPU=6 -ICPU=3
-NO MWAP -NMG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELext=7

Database: Published Applications.NA.Main:

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7: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
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9: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	453	100.0	1104	6	US-10-071-645-1
2	413	91.2	553	6	US-10-136-728-21
3	413	91.2	1876	9	US-10-765-700-70
4	290	64.0	3189	6	US-10-071-645-3
5	281	62.0	1510	6	US-09-820-649-25
6	281	62.0	1510	6	US-10-160-162-25
7	281	62.0	1510	8	US-10-936-773-25

8	259.5	57.3	1222	8	US-10-335-053-193	Sequence 193, App
9	253.5	56.0	550	7	US-10-352-574-1	Sequence 1, App1
10	245	56.1	556	7	US-09-783-590-147	Sequence 147, App
11	229	50.6	549	7	US-10-152-119-124	Sequence 124, App
12	129	43.9	869	8	US-10-363-455-28797	Sequence 28797, A
13	139	43.9	869	8	US-10-363-455-28798	Sequence 28798, A
14	139	43.9	869	9	US-10-363-483-28797	Sequence 28797, A
15	159	43.9	869	9	US-10-363-483-28798	Sequence 28798, A
16	197	43.5	869	8	US-10-363-445-29799	Sequence 29799, A
17	197	43.5	869	8	US-10-363-445-29800	Sequence 29800, A
18	197	43.5	869	9	US-10-363-483-29799	Sequence 29799, A
19	197	43.5	869	9	US-10-363-483-29800	Sequence 29800, A
20	196	43.3	255	8	US-10-491-323-3	Sequence 3, App1
21	186	41.1	2058	8	US-10-723-860-7058	Sequence 7058, App
22	175	38.6	1850	5	US-10-198-846-11350	Sequence 11350, A
23	172	38.0	600	9	US-10-956-157-7495	Sequence 7495, App
24	172	38.0	1321	6	US-10-172-118-1796	Sequence 1796, App
25	172	38.0	1321	7	US-10-342-887-1796	Sequence 1796, App
26	172	38.0	1321	9	US-10-956-157-2260	Sequence 2260, App
27	172	38.0	1321	9	US-10-631-467-450	Sequence 450, App1
28	149	32.9	129	8	US-10-491-323-5	Sequence 5, App1
29	128	28.3	474	3	US-09-918-995-26636	Sequence 26636, App
30	94	20.8	65	3	US-09-908-975-4520	Sequence 4520, App
31	83	18.3	65	3	US-09-908-975-4520	Sequence 4520, App
32	73.5	16.2	681	6	US-10-156-761-7087	Sequence 7087, App
33	73.5	16.2	9025608	6	US-10-156-761-1	Sequence 1, App1
34	72.5	16.1	2311	7	US-10-757-701-7926	Sequence 7926, App
35	72.5	16.0	101255	8	US-10-437-953-34784	Sequence 34784, App
36	72.5	16.0	101255	8	US-10-719-893-6830	Sequence 6830, App
37	71.5	15.8	654	7	US-10-724-922-427	Sequence 427, App
38	71	15.7	1351	7	US-10-437-963-10959	Sequence 10959, App
39	71	15.7	113306	6	US-10-292-798-1007	Sequence 1007, App
40	70.5	15.6	1169	3	US-09-864-761-31876	Sequence 31876, App
41	70.5	15.6	1965	3	US-09-864-761-15362	Sequence 15362, App
42	70.5	15.6	2647	7	US-10-437-963-21280	Sequence 21280, App
43	70	15.5	1452	7	US-10-424-599-80120	Sequence 80120, App
44	69.5	15.3	1755	6	US-10-369-493-36207	Sequence 36207, App
45	69.5	15.3	2836	7	US-10-437-963-51222	Sequence 51222, App

ALIGNMENTS

RESULT 1
US-10-071-645-1
; Sequence 1, Application US/10071645
; Publication No. US2003014839A1
; GENERAL INFORMATION:
; APPLICANT: Bihain, Bernard
; APPLICANT: Bouguet-Lydie
; TITLE OF INVENTION: Schizophrenia Related Gene and Protein
; PIR REFERENCE: 92.US2.CIP
; CURRENT APPLICATION NUMBER: US/10/071.645
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/223,482
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: FCT/IB01/01891
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: 87..346
US-10-071-645-1
Alignment Scores:
Pred. No.: 2.54e-57 Length: 1104
Score: 453.00 Matches: 85
Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 6
Mismatches: 0
Indels: 0
Gaps: 0

US-10-071-645-2 (1-85) x US-10-071-645-1 (1-1104)

QY 1 MetTPGluValLeuProTyrgLYAspGluLeuSerProTyrgLYAspGlyIYAsp 20
DB 87 ATGTGGAGGTGCTGCTTACCGGACGAGAACTGAGCCCTTACGGCGAGCGCGGCGAG 146
QY 21 ValGlyGlnIlePheSerCysArgLeuGlnAspThrAsnAspPheGlyAlaGlyGln 40
DB 147 GTGGGCGAGATCTTCTCTGCGCGCTGCGAGACACCACTTCTTCTGCGCGCGGCGAG 206
QY 41 AsnLYsArgProProlYSLeuGlyGlnIleGlyArgSerLYsArgValIleGlyAsp 60
DB 207 AACAAAGCGCGCGCCCAAGCTGGGCGCAATCGCGGAGCAAGCGGGTGTATTGAAGAT 266
QY 61 AsparGlyLeuAspValLeuLYsAsnMetThrAspLYsAlaProLeuValSerAsnSer 80
DB 267 GATAGAGATTGATGAGCTGCTGAAAATATGACCAAGCAAGCACTCTGTGTCTAACTCC 326
QY 81 ProlYSThrMetSer 85
DB 327 CCNAAAGCAATGAGT 341

RESULT 2
US-10-136-728-21
Sequence 21, Application US/10136728
Publication No. US20030236188A1
GENERAL INFORMATION:
APPLICANT: Splytek, Kimberly A.
APPLICANT: Li, Li
APPLICANT: Edinger, Shlomit R.
APPLICANT: Stone, David J.
APPLICANT: Guo, Xiaojia
APPLICANT: Anderson, David W.
APPLICANT: Patuvarajan, Meera
APPLICANT: Gerlach, Valerie L.
APPLICANT: Taupier, Raymond J.
APPLICANT: Pena, Carol E.A.
APPLICANT: Padigaru, Murajidhara
APPLICANT: Kekuda, Ramesh
APPLICANT: Gorman, Linda
APPLICANT: Zernusen, Bryan D.
APPLICANT: MacDougall, John R.
APPLICANT: Mezes, Peter S.
APPLICANT: Perman, John A.
APPLICANT: Zhong, Mel
TITLE OF INVENTION: NO. US20030236188A1 Human Proteins, Polynucleotides Encoding TH
FILE REFERENCE: 21402-347 D (Cura 647 Other)
CURRENT APPLICATION NUMBER: US/10/136,728
PRIOR FILING DATE: 2002-05-01
PRIOR APPLICATION NUMBER: 60/288,395
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 60/289,087
PRIOR FILING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: 60/289,619
PRIOR FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: 60/289,818
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 60/289,817
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 60/290,194
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/290,753
PRIOR FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 60/291,189
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/292,374
PRIOR FILING DATE: 2001-05-21

PRIOR APPLICATION NUMBER: 60/293,107
PRIOR FILING DATE: 2001-05-23
Remainder of Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 21
LENGTH: 553
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (72) .. (306)
US-10-136-728-21

Alignment Scores:

Pred. No.: 1.04e-51 Length: 553
Score: 413.00 Matches: 84
Percent Similarity: 96.6% Conservative: 0
Best Local Similarity: 96.6% Mismatch: 1
Query Match: 91.2% Indels: 2
DB: 6 Gaps: 0

US-10-071-645-2 (1-85) x US-10-136-728-21 (1-553)

QY 1 MetTPGluValLeuProTyrgLYAspGluLeuSerProTyrgLYAspGlyIYAsp 20
DB 72 ATGTGGAGGTGCTGCTTACCGGACGAGAACTGAGCCCTTACGGCGAGCGCGGCGAG 131
QY 21 ValGlyGlnIlePheSerCysArgLeuGlnAspThrAsnAspPheGlyAlaGlyGln 40
DB 132 GTGGGCGAGATCTTCTCTGCGCGCTGCGAGACACCACTTCTTCTGCGCGCGGCGAG 191
QY 41 AsnLYsArgProProlYSLeuGlyGlnIleGlyArgSerLYsArgValIleGlyAsp 60
DB 192 AACAAAGCGCGCGCCCAAGCTGGGCGCAATCGCGGAGCAAGCGGGTGTATTGAAGAT 251
QY 61 AsparGlyLeuAspValLeuLYsAsnMetThrAspLYsAlaProLeuValSerAsnSer 80
DB 252 GATAGAGATTGATGAGCTGCTGAAAATATGACCAAGCAAGCACTCTGTGTCTAACTC 311
QY 80 ProlYSThrMetSer 85
DB 312 CCCNAAAGCAATGAGT 328

RESULT 3

US-10-765-700-70
Sequence 70, Application US/10765700
Publication No. US20050130171A1
GENERAL INFORMATION:
APPLICANT: Loring, Jeanne P.
APPLICANT: Edwards, Carla M.
APPLICANT: Tingley, Deborah W.
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
FILE REFERENCE: PA-0024 US
CURRENT APPLICATION NUMBER: US/10/765,700
PRIOR FILING DATE: 2004-01-26
PRIOR APPLICATION NUMBER: US/09/566,921
PRIOR FILING DATE: PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL Program
SEQ ID NO 70
LENGTH: 1876
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 234151.1
FEATURE:
NAME/KEY: ununre
LOCATION: 1360, 1362-1391, 1864
OTHER INFORMATION: a, t, c, g, or other
US-10-765-700-70

Alignment Scores:

Pred. No.: 5e-51 Length: 1876
 Score: 413.00 Matches: 84
 Percent Similarity: 96.6% Conservative: 0
 Best Local Similarity: 96.6% Mismatches: 1
 Query Match: 91.2% Indels: 2
 DB: 9 Gaps: 0

US-10-071-645-2 (1-85) x US-10-765-700-70 (1-1876)

QY 1 MetTpgjUvAlleuProTygIyAspQjUlyLeuSerProTygIyAspQjUlyAsp 20
 Db 355 ATGTGCGAGGTGTGCTGCTGACGCGCAGAGAACTGAGCCCTTGCGCGAGCGCGCGC 414
 QY 21 ValGlyGlnIlePheSerCyArGLeuGlnAspThraAsmPhePheGlyAlaGlyGln 40
 Db 415 GTGGGCGCAGATCTTCTCTGCGCGCTGCGAGGACCAACAACTTCTTCTGCGCGCGCG 474
 QY 41 AenlysaGrProProlysLeuGlyGlnIleGlyArGSerLyArGValIleGlyAsp 60
 Db 475 AACCAAGCGCGCGCGCAAGCTGGGCGCAAGTCGGCGGAGCAAGCGGCTTTGTTATTAAGT 534
 QY 61 AspaTrgIleAspaPylleuAspMetThraPylAspAlaPro-LeuValSerAsp 80
 Db 535 GATGAGATTGATGATCTGCTGTAATAATATGACCAAGCAAGCTCTGATGCTTACTC 594
 QY 80 r-ProlystThrmeter 85
 Db 595 CCCCAGAGCAATGAGT 611

RESULT 4
 US-10-071-645-3

Sequence 3, Application US/10071645
 Publication No. US20030148389A1
 GENERAL INFORMATION:
 APPLICANT: Bihain, Bernard
 APPLICANT: Bouret, Barbara
 APPLICANT: Bouguet, Lydie
 TITLE OF INVENTION: Schizophrenia Related Gene and Protein
 FILE REFERENCE: 92.US2.CIP
 CURRENT APPLICATION NUMBER: US/10/071,645
 PRIOR FILING DATE: 2002-02-06
 PRIOR APPLICATION NUMBER: 60/223,482
 PRIOR FILING DATE: 2000-08-07
 PRIOR APPLICATION NUMBER: PCT/IB01/01891
 PRIOR FILING DATE: 2001-07-26
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: Patent.pm
 SEQ ID NO 3
 LENGTH: 3189
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-071-645-3

Alignment Scores:

Pred. No.: 2.75e-32 Length: 3189
 Score: 290.00 Matches: 54
 Percent Similarity: 98.2% Conservative: 0
 Best Local Similarity: 98.2% Mismatches: 1
 Query Match: 64.0% Indels: 0
 DB: 6 Gaps: 0

US-10-071-645-2 (1-85) x US-10-071-645-3 (1-3189)

QY 1 MetTpgjUvAlleuProTygIyAspQjUlyLeuSerProTygIyAspQjUlyAsp 20
 Db 499 ATGTGCGAGGTGTGCTGCTGACGCGCAGAGAACTGAGCCCTTGCGCGAGCGCGCGC 558
 QY 21 ValGlyGlnIlePheSerCyArGLeuGlnAspThraAsmPhePheGlyAlaGlyGln 40
 Db 559 GTGGGCGCAGATCTTCTCTGCGCGCTGCGAGGACCAACAACTTCTTCTGCGCGCGCG 618
 QY 41 AenlysaGrProProlysLeuGlyGlnIleGlyArGSerLyArGValIleGlyAsp 55

Db 619 AACCAAGCGCGCGCGCAAGCTGGGCGCAAGTCGGCGGAGCAAGCGG 663

RESULT 5

US-09-820-649-25
 Sequence 25, Application US/09820649
 Publication No. US20030199683A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: 83 Human Secreted Proteins

FILE REFERENCE: P2012P1

CURRENT APPLICATION NUMBER: US/09/820,649

PRIOR FILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: US/09/236,557

PRIOR FILING DATE: 1999-01-26

PRIOR APPLICATION NUMBER: PCT/US98/15949

PRIOR FILING DATE: 1998-07-29

PRIOR APPLICATION NUMBER: 60/054,212

PRIOR FILING DATE: 1997-07-30

PRIOR APPLICATION NUMBER: 60/054,209

PRIOR FILING DATE: 1997-07-30

PRIOR APPLICATION NUMBER: 60/054,234

PRIOR FILING DATE: 1997-07-30

PRIOR APPLICATION NUMBER: 60/054,218

PRIOR FILING DATE: 1997-07-30

PRIOR APPLICATION NUMBER: 60/054,214

PRIOR FILING DATE: 1997-07-30

PRIOR APPLICATION NUMBER: 60/054,236

PRIOR FILING DATE: 1997-07-30

PRIOR APPLICATION NUMBER: 60/054,215

PRIOR FILING DATE: 1997-07-30

PRIOR APPLICATION NUMBER: 60/054,211

PRIOR FILING DATE: 1997-07-30

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 353

SOFTWARE: Patent in Ver. 2.0

SEQ ID NO 25

LENGTH: 1510

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (39)

OTHER INFORMATION: n equals a,t,g, or c

US-09-820-649-25

Alignment Scores:

Pred. No.: 2.35e-31 Length: 1510
 Score: 281.00 Matches: 64
 Percent Similarity: 92.8% Conservative: 0
 Best Local Similarity: 92.8% Mismatches: 3
 Query Match: 62.0% Indels: 3
 DB: 3 Gaps: 0

US-10-071-645-2 (1-85) x US-09-820-649-25 (1-1510)

QY 19 GlyAspValIleGlnIlePheSerCyArGLeuGlnAspThraAsmPhePheGlyAla 38
 Db 2 GCGCAGGTGGGCGCAGATCTTCTCTGCGCGCTGCAAGNCAACCAACTTCTTCTGCGCGC 61
 QY 39 GlyGlnAsnlysaGrProProlysLeuGlyGlnIleGlyArGSerLyArGValIle 58
 Db 62 GCGCGAAGCAAGCGCGCGCAAG-CTGGCGCAAGATCGGCGGAGCAAGCGGCTTTATTT 120
 QY 59 GluAspaPylleuAspMetThraPylAspAlaPro-LeuValSer 78
 Db 121 GAAGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 QY 78 rAsnser-ProlystThrmeter 85
 Db 181 TAACTCCCGCAAGCAATGAGT 203

RESULT 6

US-10-160-162-25

```
Sequence 25, Application US/10160162
Publication No. US20030166541A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 83 Human Secreted Proteins
FILE REFERENCE: P2012P2
CURRENT APPLICATION NUMBER: US/10/160,162
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: 60/295,558
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 09/236,557
PRIOR FILING DATE: 1998-01-26
PRIOR APPLICATION NUMBER: PCT/US98/15949
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: 60/054,212
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,209
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,234
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,218
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,214
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,236
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,215
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,211
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,217
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,213
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/055,968
PRIOR FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: 60/055,969
PRIOR FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: 60/055,972
PRIOR FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: 60/056,561
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,534
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,729
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,543
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,727
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,554
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,730
PRIOR FILING DATE: 1997-08-19
NUMBER OF SEQ ID NOS: 353
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
LENGTH: 1510
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (39)
OTHER INFORMATION: n equals a,t,g, or c
US-10-160-162-25

Alignment Scores:
Pred. No.: 2,35e-31 Length: 1510
Score: 281.00 Matches: 64
Percent Similarity: 92.88 Conservative: 0
Best Local Similarity: 92.88 Mismatches: 3
Query Match: 62.0% Indels: 3
DB: 6 Gaps: 0

Sequence 7
US-10-936-773-25
Publication US/10936773
Publication No. US20050037467A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 83 Human Secreted Proteins
FILE REFERENCE: P2012P2
CURRENT APPLICATION NUMBER: US/10/936,773
CURRENT FILING DATE: 2004-09-09
PRIOR APPLICATION NUMBER: US/10/160,162
PRIOR FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: 60/295,558
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 09/236,557
PRIOR FILING DATE: 1999-01-26
PRIOR APPLICATION NUMBER: PCT/US98/15949
PRIOR FILING DATE: 1998-07-29
PRIOR APPLICATION NUMBER: 60/054,212
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,209
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,234
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,218
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,214
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,236
PRIOR FILING DATE: 1997-07-30
Remainding prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 353
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
LENGTH: 1510
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (39)
OTHER INFORMATION: n equals a,t,g, or c
US-10-936-773-25

Alignment Scores:
Pred. No.: 2,35e-31 Length: 1510
Score: 281.00 Matches: 64
Percent Similarity: 92.88 Conservative: 0
Best Local Similarity: 92.88 Mismatches: 3
Query Match: 62.0% Indels: 3
DB: 8 Gaps: 0

US-10-071-645-2 (1-85) x US-10-160-162-25 (1-1510)
OY 19 GlyAspValGlyGlnIlePheSerCysArgLeuGlnAspThrAsnAsnPheGlyAla 38
Db 2 GGGCAGCGGGCCAGATCTCTCTGCGCGCGAGNACCAACAACTCTTCGGCGCC 61
OY 33 GlyGlnAsnLysArgProGlyLeuGlyGlnIleGlyArgSerLysArgValIle 58
Db 62 GGGCAGAAACAGCGCGCGCAAG-CTGGCGAGATCGCGCGAGCGAGCGGGTGTAT 120
OY 59 GluAspAspArgIleAspAspValLeuLysAsnMetThrAspLysAlaPro-LeuValSe 78
Db 121 GAAGATGATGAGTGTATGACCTGTGAAAAATATGACGACGACGACCTCTGATGTC 180
OY 78 rAnser-ProLysThrMetSer 85
Db 181 TAATCTCCCAAGACATGAGT 203

RESULT 7
US-10-936-773-25
Sequence 25, Application US/10936773
Publication No. US20050037467A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 83 Human Secreted Proteins
FILE REFERENCE: P2012P2
CURRENT APPLICATION NUMBER: US/10/936,773
CURRENT FILING DATE: 2004-09-09
PRIOR APPLICATION NUMBER: US/10/160,162
PRIOR FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: 60/295,558
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 09/236,557
PRIOR FILING DATE: 1999-01-26
PRIOR APPLICATION NUMBER: PCT/US98/15949
PRIOR FILING DATE: 1998-07-29
PRIOR APPLICATION NUMBER: 60/054,212
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,209
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,234
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,218
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,214
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,236
PRIOR FILING DATE: 1997-07-30
Remainding prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 353
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
LENGTH: 1510
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (39)
OTHER INFORMATION: n equals a,t,g, or c
US-10-936-773-25

Alignment Scores:
Pred. No.: 2,35e-31 Length: 1510
Score: 281.00 Matches: 64
Percent Similarity: 92.88 Conservative: 0
Best Local Similarity: 92.88 Mismatches: 3
Query Match: 62.0% Indels: 3
DB: 8 Gaps: 0

US-10-071-645-2 (1-85) x US-10-936-773-25 (1-1510)
OY 19 GlyAspValGlyGlnIlePheSerCysArgLeuGlnAspThrAsnAsnPheGlyAla 38
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Db      2  GGCACCGGCGCCAGATCTTCTCCGCGCTGAGGACCAACCTTCTGCGGCC 61
Qy      39  GYGINAENLYSARPRPROLYSLEUGLYGINILEGIVARSERLYSARGLVALIIE 58
Db      62  GGGCAAGAACAGAGCGCGCCGCAAG-CTGGGCGAAGATCGCGCGAGCAAGCGGCTGTATT 120
Qy      59  GIUASPAPATGIIAASPAPVALIENLYSASMETTHIASPLYSALAPRO-LEUVALISE 78
Db      121  GAAGATATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
Qy      78  RASNER-PROLYSTIRMETSER 85
Db      181  TAACCTCCCGCAAGACATGAGT 203

RESULT 8
US-10-335-053-193
; Sequence 193, Application US/10335053
; Publication No. US20040241653A1
; GENERAL INFORMATION:
; APPLICANT: Quark Biotech, Inc.
; TITLE OF INVENTION: Methods for identifying marker genes for cancer
; FILE REFERENCE: 68733-A, 070/US1
; CURRENT APPLICATION NUMBER: US/10/335,053
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: 60/345,317
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 193
; LENGTH: 1222
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (746)..(746)
; OTHER INFORMATION: n is a, c, g, or t
US-10-335-053-193

Alignment Scores:
Pred. No.: 3e-28      Length: 1222
Score: 259.50      Matches: 51
Percent Similarity: 78.2%      Conservative: 10
Best Local Similarity: 65.4%      Mismatches: 12
Query Match: 57.3%      Indels: 5
DB: 8      Gaps: 2

US-10-071-645-2 (1-85) x US-10-335-053-193 (1-1222)
Qy      1  METTPGLVALLLEUPROYTYGIVASPOLYLSLEUSERPROTYGIVY-----ASP 17
Db      32  ATGTCGAGATCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 91
Qy      18  GYGLYASPVALIGYGINILEPHESERYSARLEUGLINASPTTHASANPHEPHEGLY 37
Db      92  GGTTCGACCTCTCT-----TTACGCTCGCGCGCTGCGAGACCAACCTCTTCTTGGCT 145
Qy      38  AIAGLYINAMLYSARPRPROLYSLEUGLYGINILEGIVARSERLYSARGLVALIIE 57
Db      146  GGCACCGGCGCCAGAGCGCGCCGCAAG-CTGGGCGAAGATCGCGCGAGCAAGCGGCTGT 205
Qy      58  IIEGIUASPAPATGIIAASPAPVALIENLYSASMETTHIASPLYSALAPRO 75
Db      206  ATCGAGATGACCGGATGACGATGACGATGACGATGACGATGACGATGACGATGACGATG 259

RESULT 9
US-10-362-674-1
; Sequence 1, Application US/10362674
; Publication No. US20040086973A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: Calmodulin dependent kinase inhibitor
; FILE REFERENCE: CAMKIIINXMS

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; CURRENT APPLICATION NUMBER: US/10/362,674
; CURRENT FILING DATE: 2003-08-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (134)..(373)
US-10-362-674-1

Alignment Scores:
Pred. No.: 8.55e-28      Length: 550
Score: 253.50      Matches: 50
Percent Similarity: 76.9%      Conservative: 10
Best Local Similarity: 64.1%      Mismatches: 13
Query Match: 56.0%      Indels: 5
DB: 7      Gaps: 2

US-10-071-645-2 (1-85) x US-10-362-674-1 (1-550)
Qy      1  METTPGLVALLLEUPROYTYGIVASPOLYLSLEUSERPROTYGIVY-----ASP 17
Db      134  ATGTCGAGATCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 193
Qy      18  GYGLYASPVALIGYGINILEPHESERYSARLEUGLINASPTTHASANPHEPHEGLY 37
Db      194  GGTTCGACCTCTCTC-----TTACGCTCGCGCGCTGCGAGACCAACCTCTTCTTGGC 247
Qy      38  AIAGLYINAMLYSARPRPROLYSLEUGLYGINILEGIVARSERLYSARGLVALIIE 57
Db      248  GGCACCGGCGCCAGAGCGCGCCGCAAG-CTGGGCGAAGATCGCGCGAGCAAGCGGCTGT 307
Qy      58  IIEGIUASPAPATGIIAASPAPVALIENLYSASMETTHIASPLYSALAPRO 75
Db      308  ATCGAGATGACCGGATGACGATGACGATGACGATGACGATGACGATGACGATGACGATG 361

RESULT 10
US-09-783-590-147
; Sequence 147, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillion, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO. 6,2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 147
; LENGTH: 356
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)
; OTHER INFORMATION: n equals a,c,g, or c
; NAME/KEY: misc_feature
; LOCATION: (26)
; OTHER INFORMATION: n equals a,c,g, or c
; NAME/KEY: misc_feature
; LOCATION: (50)
; OTHER INFORMATION: n equals a,c,g, or c

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NAME/KEY: misc feature
LOCATION: (110)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (113)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (121)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (135)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (155)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (165)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (171)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (182)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (197)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (201)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (204)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (236)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (254)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (255)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (256)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (258)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (260)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (263)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (264)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (265)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (270)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (304)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (307)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (312)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature

LOCATION: (316)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (318)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (323)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (324)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (336)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (340)
OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-147
Alignment Scores:
Pred. No.: 9,21e-27 Length: 356
Score: 245.00 Matches: 58
Percent Similarity: 72.64 Conservative: 3
Best Local Similarity: 69.04 Mismatches: 19
Query Match: 54.14 Indels: 4
DB: 3 Gaps: 2
US-10-071-645-2 (1-85) x US-09-783-590-147 (1-356)
QY 3 GluValLeuProTyrGlyAspGluValLeuSerProTyrGlyAspGlyValGly 22
DB 51 AAGTGTCTGCTCCCTAAGCGCAAGAGCTGAGCCCTTACGCGCAAGCGGAGTGGG 110
QY 23 GluIlePheSerCysArgLeuGlnAspThrAsnAspPheGlyValGlyAsnLys 42
DB 111 CAAATCTCTTCTGCTGCTGCGCGCGACCAACACTTCTTCCGAGCCGCGCAACAG 170
QY 43 ArgProProLysLeuGlyGlnIleGlyArg-SerLysArgValValIleGlu-AspAsp 62
DB 171 NGGCGCTCCCAACAGTGGCGCAATGCGAGNAGGCGGTGTATTGAAGAATGGTA 230
QY 62 rGlleAspAspValLeu---LysAsnMetThrAspLysAlaProLeu---ValSerAsn 80
DB 231 GGATTNATGACGTGCTG3AAAANNNTNGCCNNNAAGNACCTTCTGATGTTTAAAT 290
QY 80 exProLys 82
DB 291 CCCCNA 298
RESULT 11
US-10-152-319A-124/c
Sequence 124, Application US/10152319A
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: H198, Brandon
APPLICANT: Castle, Arthur
APPLICANT: Blaschoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,807


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; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/330,462
; PRIOR FILING DATE: 2001-10-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 124
; LENGTH: 549
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. M858621
US-10-152-319A-124

Alignment Scores:
Pred. No.: 4,036-24 Length: 549
Score: 229,100 Matches: 42
Percent Similarity: 97.7% Conservative: 1
Best Local Similarity: 95.5% Mismatches: 1
Query Match: 50.6% Indels: 0
DB: 7 Gaps: 0

US-10-071-645-2 (1-85) x US-10-152-319A-124 (1-549)

QY 1 MetTpgUuVallauProTyrGlyAspGluYsleuSerProTyrGlyAspGlyGlyAsp 20
Db 132 ATGTGAGAGGTCTGCTGCGACGACGACGACGACGACGACGACGACGACGACGACG 73

QY 21 ValGlyGlnIlePheSerCysArgLeuGlnAspThrAsnAspPhePheGlyAlaGlyGln 40
Db 72 GTGGGCGCAGATCTTCTGCGCGCTGCGACGACGACGACGACGACGACGACGACGACG 13

RESULT 12
US-10-363-345A-29797/c
; Sequence 29797, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christiaan Piepenbrock
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; CURRENT APPLICATION NUMBER: US/10/363,345A
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO: 29797
; LENGTH: 869
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-29797

Alignment Scores:
Pred. No.: 2,296-19 Length: 869
Score: 199,000 Matches: 38
Percent Similarity: 81.1% Conservative: 5
Best Local Similarity: 71.7% Mismatches: 10
Query Match: 43.9% Indels: 0
DB: 8 Gaps: 0

RESULT 13
US-10-363-345A-29798
; Sequence 29798, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christiaan Piepenbrock
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; CURRENT APPLICATION NUMBER: US/10/363,345A
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO: 29798
; LENGTH: 869
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-29798

Alignment Scores:
Pred. No.: 2,296-19 Length: 869
Score: 199,000 Matches: 38
Percent Similarity: 81.1% Conservative: 5
Best Local Similarity: 71.7% Mismatches: 10
Query Match: 43.9% Indels: 0
DB: 8 Gaps: 0

US-10-071-645-2 (1-85) x US-10-363-345A-29798 (1-869)

QY 3 GluValLeuProTyrGlyAspGluYsleuSerProTyrGlyAspGlyGlyAspValGly 22
Db 456 AATAATCTAACCCTTACGACGACGACGACGACGACGACGACGACGACGACGACG 515

QY 23 GlnIlePheSerCysArgLeuGlnAspThrAsnAspPhePheGlyAlaGlyGlnAsn 42
Db 516 CAATCTCTCTCTTACGCGCTTACGACGACGACGACGACGACGACGACGACGACGAC 575

QY 43 ArgProProYsleuGlyGlnIleGlyArgSerYsArg 55
Db 576 CGACCGCCCAAACTTAACCAATCGACGACGACGACGACGACGACGACGACGACGAC 614

RESULT 14
US-10-363-483A-29797/c
; Sequence 29797, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christiaan Piepenbrock
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
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DB: 8 Gaps: 0
US-10-071-645-2 (1-85) x US-10-363-345A-29797 (1-869)
QY 3 GluValLeuProTyrGlyAspGluYsleuSerProTyrGlyAspGlyGlyAspValGly 22
Db 414 AATAATCTAACCCTTACGACGACGACGACGACGACGACGACGACGACGACGACG 355
QY 23 GlnIlePheSerCysArgLeuGlnAspThrAsnAspPhePheGlyAlaGlyGlnAsn 42
Db 354 CAATCTCTCTCTTACGCGCTTACGACGACGACGACGACGACGACGACGACGACGAC 295
QY 43 ArgProProYsleuGlyGlnIleGlyArgSerYsArg 55
Db 294 CGACCGCCCAAACTTAACCAATCGACGACGACGACGACGACGACGACGACGACGAC 256

RESULT 13
US-10-363-345A-29798
; Sequence 29798, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christiaan Piepenbrock
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; CURRENT APPLICATION NUMBER: US/10/363,345A
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO: 29798
; LENGTH: 869
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-29798

Alignment Scores:
Pred. No.: 2,296-19 Length: 869
Score: 199,000 Matches: 38
Percent Similarity: 81.1% Conservative: 5
Best Local Similarity: 71.7% Mismatches: 10
Query Match: 43.9% Indels: 0
DB: 8 Gaps: 0

US-10-071-645-2 (1-85) x US-10-363-345A-29798 (1-869)

QY 3 GluValLeuProTyrGlyAspGluYsleuSerProTyrGlyAspGlyGlyAspValGly 22
Db 456 AATAATCTAACCCTTACGACGACGACGACGACGACGACGACGACGACGACGACG 515

QY 23 GlnIlePheSerCysArgLeuGlnAspThrAsnAspPhePheGlyAlaGlyGlnAsn 42
Db 516 CAATCTCTCTCTTACGCGCTTACGACGACGACGACGACGACGACGACGACGACGAC 575

QY 43 ArgProProYsleuGlyGlnIleGlyArgSerYsArg 55
Db 576 CGACCGCCCAAACTTAACCAATCGACGACGACGACGACGACGACGACGACGACGAC 614

RESULT 14
US-10-363-483A-29797/c
; Sequence 29797, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christiaan Piepenbrock
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
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; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 29797
; LENGTH: 869
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 29797
US-10-363-483A-29797

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```

Alignment Scores:
Pred. No.: 2.29e-19      Length: 869
Score: 199.00           Matches: 38
Percent Similarity: 81.1% Conservative: 5
Best Local Similarity: 71.7% Mismatches: 10
Query Match: 43.9%      Indels: 0
DB: 9                    Gaps: 0

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US-10-071-645-2 (1-85) x US-10-363-483A-29797 (1-869)

```

Qy 3 GluValLeuProTyrGlyAspGluIleuSerProTyrGlyAspGlyGlyAspValGly 22
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 414 AAATACCTACCTACGACGACGAACTAAACCCCTACGACGACGACGACGACGTTAAC 355

Qy 23 GlnIlePheSerCysArgLeuGlnAspThrAsnAsnPhenheGlyAlaGlyGlnAsnLys 42
    ||||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 354 CAATCTTCTCTACCGCTTCAAAACACCAACTTCTTCAACCGCAACAAACAAA 295

Qy 43 ArgProProIysLeuGlnIleGlyArgSerLysArg 55
    ||||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 294 CGACCGCCCAACTAAACCAATCGACCGCAACAAACGA 256

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RESULT 15

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US-10-363-483A-29798
; Sequence 29798, Application US/10363483A
; Publication NO. US2005064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 29798
; LENGTH: 869
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 29798
US-10-363-483A-29798

```

```

Alignment Scores:
Pred. No.: 2.29e-19      Length: 869
Score: 199.00           Matches: 38
Percent Similarity: 81.1% Conservative: 5
Best Local Similarity: 71.7% Mismatches: 10
Query Match: 43.9%      Indels: 0
DB: 9                    Gaps: 0

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US-10-071-645-2 (1-85) x US-10-363-483A-29798 (1-869)

```

Qy 3 GluValLeuProTyrGlyAspGluIleuSerProTyrGlyAspGlyGlyAspValGly 22
    : : : : : : : : : : : : : : : : : : : : : : : :
Db 456 AAATACCTACCTACGACGACGAACTAAACCCCTACGACGACGACGACGACGTTAAC 515

Qy 23 GlnIlePheSerCysArgLeuGlnAspThrAsnAsnPhenheGlyAlaGlyGlnAsnLys 42
    ||||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 516 CAATCTTCTCTACCGCTTCAAAACACCAACTTCTTCAACCGCAACAAACAAA 575

```

```

Qy 43 ArgProProIysLeuGlnIleGlyArgSerLysArg 55
    ||||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 576 CGACCGCCCAACTAAACCAATCGACCGCAACAAACGA 614

```

Search completed: March 9, 2006, 00:41:07
Job time : 795 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: March 8, 2006, 23:59:34 ; Search time 324 Seconds
(without alignments)
605.309 Million cell updates/sec

Title: US-10-071-645-2
Perfect score: 453

Sequence: 1 MWEVLPYGDKEKSPYGDGD.....VLKMTDKAPLVNSPKTWS 85

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7673375 segs, 115364844 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame.p2n.model -DEV=xlh
-Q=abses/ABSWEB.spool/US10071645/runat_08032006_115130_4832/app_query.fasta.1
-DB=Published Applications NA.New -OPMT=fastcap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=bl0sum62
-TRANS-human40.cdi -LIST=45 -MODE=LOCAL -ALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORP=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abs804
-USER=US10071645 @CNI 1.1431 @runat_08032006_115130_4832 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV TIMEOUT=120
-MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
1	71.5	15.8	447 8 US-10-793-626-3121	Sequence 3121, Ap
2	71.5	15.8	4218 8 US-10-793-626-4205	Sequence 4205, Ap
3	70.5	15.6	771 7 US-10-932-182A-4581	Sequence 4581, Ap
4	70.5	15.6	771 7 US-10-932-182A-4581	Sequence 4581, Ap

5	69	15.2	531 6 US-09-925-065A-600042	Sequence 600042,
6	68	15.0	2700 12 US-11-186-282-33	Sequence 33, Appl
7	68	15.0	2710 7 US-10-764-818A-17	Sequence 17, Appl
8	68	15.0	2713 7 US-10-764-818A-18	Sequence 18, Appl
9	68	15.0	2713 7 US-10-764-818A-21	Sequence 21, Appl
10	68	15.0	2716 7 US-10-764-818A-19	Sequence 19, Appl
11	68	15.0	2716 7 US-10-764-818A-20	Sequence 20, Appl
12	68	15.0	2716 12 US-11-186-282-27	Sequence 27, Appl
13	68	15.0	2716 12 US-11-186-282-28	Sequence 28, Appl
14	68	15.0	2716 12 US-11-186-282-29	Sequence 29, Appl
15	68	15.0	2716 12 US-11-186-282-31	Sequence 31, Appl
16	68	15.0	2721 12 US-11-186-282-33	Sequence 33, Appl
17	68	15.0	2721 12 US-11-186-282-34	Sequence 34, Appl
18	68	15.0	2722 12 US-11-186-282-23	Sequence 23, Appl
19	68	15.0	2725 7 US-10-764-818A-30	Sequence 30, Appl
20	68	15.0	2725 12 US-11-186-282-24	Sequence 24, Appl
21	68	15.0	2725 12 US-11-186-282-25	Sequence 25, Appl
22	68	15.0	2725 12 US-11-186-282-32	Sequence 32, Appl
23	68	15.0	2739 7 US-10-764-818A-28	Sequence 28, Appl
24	68	15.0	2739 12 US-11-186-282-30	Sequence 30, Appl
25	67.5	14.9	9585 12 US-11-082-554A-474	Sequence 474, App
26	66	14.8	323 7 US-10-764-818A-7	Sequence 7, Appl
27	66	14.6	1482 12 US-11-186-282-15	Sequence 15, Appl
28	66	14.6	1482 7 US-10-932-182A-605	Sequence 605, App
29	66	14.6	1482 7 US-10-932-182A-605	Sequence 605, App
30	66	14.6	1761 7 US-10-932-182A-8163	Sequence 8163, A
31	66	14.6	1761 7 US-10-932-182A-8163	Sequence 8163, A
32	66	14.6	3039 7 US-10-932-182A-3076	Sequence 3076, Ap
33	66	14.6	3039 7 US-10-932-182A-3076	Sequence 3076, Ap
34	66	14.6	3534 7 US-10-764-818A-11	Sequence 11, Appl
35	66	14.6	3534 7 US-10-764-818A-12	Sequence 12, Appl
36	66	14.6	3534 7 US-10-764-818A-13	Sequence 13, Appl
37	66	14.6	3534 7 US-10-764-818A-14	Sequence 14, Appl
38	66	14.6	3534 7 US-10-764-818A-15	Sequence 15, Appl
39	66	14.6	3534 7 US-10-764-818A-29	Sequence 29, Appl
40	66	14.6	3534 12 US-11-186-282-22	Sequence 22, Appl
41	66	14.6	3999 9 US-11-242-459-7	Sequence 7, Appl
42	66	14.6	4260 7 US-10-764-818A-16	Sequence 16, Appl
43	65.5	14.5	1344 7 US-10-932-182A-80465	Sequence 80465, A
44	65.5	14.5	1344 7 US-10-932-182A-80465	Sequence 80465, A
45	65	14.3	775 6 US-09-925-065A-42289	Sequence 42289, A

ALIGNMENTS

RESULT 1
US-10-793-626-3121
Sequence 3121, Application US/10793626
Publication No. US20050253478A1
GENERAL INFORMATION:
APPLICANT: KIMBERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/10/793,626
PRIORITY FILING DATE: 2004-03-04
PRIORITY APPLICATION NUMBER: 60/164,258
PRIORITY FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3121
LENGTH: 447
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-3121
Alignment Scores:
Pred. No.: 3.54
Score: 71.50
Percent Similarity: 52.5%
Best Local Similarity: 31.1%
Length: 447
Matches: 19
Conservative: 13
Mismatches: 20

Query Match: 15.8% Indels: 9
DB: 8 Gaps: 2

US-10-071-645-2 (1-85) x US-10-793-626-3121 (1-447)

QY 21 ValGlyGlnIlePheSerCysArgLeuGlnAspThrAsnAspPheGlyAlaGlyGln 40
169 ATGGGTAATTAGCGATGCTCATGTTAGAGATTAAATTAAC-----GCTATTAGA 219
DB 41 AsnValArgProProlysLeuGlyGlnIleGlyArgSerLeuArgValIleGluAsp 60
220 AATAAAGTTTACCACTGATA-----AAAGAAGTCATTGAGAGAGAT 261

QY 61 AspArgIleAspAspValIleuLysAsnMetThrAspLysAlaProLeuValSerAsnSer 80
262 GAAGATATTGATGATTATATACGTTAAACATGCTCAATACCAAGTACTTAAATGATAATGAC 321
DB 81 Pro 81
322 CCA 324

RESULT 2
US-10-793-626-4205
Sequence 4205, Application US/10793626
Publication No. US20050253478A1
GENERAL INFORMATION:
APPLICANT: KIMBERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
NUMBER OF SEQ ID NOS: 44/72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4205
LENGTH: 4218
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-4205

Alignment Scores:
Pred. No.: 48 Length: 4218
Score: 71.50 Matches: 19
Percent Similarity: 52.5% Conservative: 13
Best Local Similarity: 31.1% Mismatches: 20
Query Match: 15.8% Indels: 2
Gaps: 2

US-10-071-645-2 (1-85) x US-10-793-626-4205 (1-4218)

QY 21 ValGlyGlnIlePheSerCysArgLeuGlnAspThrAsnAspPheGlyAlaGlyGln 40
3103 ATGGGTAATTAGCGATGCTCATGTTAGAGATTAAATTAAC-----GCTATTAGA 3153
DB 41 AsnValArgProProlysLeuGlyGlnIleGlyArgSerLeuArgValIleGluAsp 60
3154 AATAAAGTTTACCACTGATA-----AAAGAAGTCATTGAGAGAGAT 3195

QY 61 AspArgIleAspAspValIleuLysAsnMetThrAspLysAlaProLeuValSerAsnSer 80
3196 GAAGATATTGATGATTATATACGTTAAACATGCTCAATACCAAGTACTTAAATGATAATGAC 3255
DB 81 Pro 81
3256 CCA 3258

RESULT 3
US-10-932-182A-4581
Sequence 4581, Application US/10932182A

Publication No. US20060046253A1
GENERAL INFORMATION:
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIRO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 030685-043
CURRENT APPLICATION NUMBER: US/10/932,182A
CURRENT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4581
LENGTH: 771
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-10-932-182A-4581

Alignment Scores:
Pred. No.: 9.14 Length: 771
Score: 70.50 Matches: 26
Percent Similarity: 35.5% Conservative: 18
Best Local Similarity: 21.0% Mismatches: 35
Query Match: 15.6% Indels: 45
Gaps: 4

US-10-071-645-2 (1-85) x US-10-932-182A-4581 (1-771)

QY 7 TyrGlyAspGlyIleuLysLeuSerProTyrGlyAspGlyIleAspVal----- 21
301 TATGACCAATCGGAATTCCTCCAGCTTATACGGAACGAGATCAACAAGATACATC 360
DB 22 -----GlyGlnIlePheSerCysArgLeuGlnAspThrAsnAspPheGlyAla 38
361 TTRCAAAAAGGGAGAGATTACCAACCCAGATATGCTGACCGCATTTTTCGTA 420
QY 39 GlyGlnAsnLysArgProProlysLeuGly-----GlnIleGlyArgSerLeuArg 55
421 CCGCAAGTAGAGAGAGAGCTGCTGCTGATATATAGCTCAAGCAAGTATCCAGCAC 480
DB 56 ValVal-----IleGluAsp 60
481 TCGATTGGAGCTATGAAGATATCTCTAATTTCGACAGAGAAAACATGTTACGAT 64
QY 61 AspArgIleAsp----- 64
541 GATVATGCTTGACATCAACTCAACAACGGTAGCAATATAGAGAAATGCGATTACAT 600
DB 65 -----AspValIleuLysAsnMetThrAspLysAlaProLeuValSerAsnSerPro 81
601 GAAACTTCTCCGTTATTAAGAAATGCGAGTACTAAAGCTGAGTATCATTAATACCCCT 660

QY 82 LysThrMetSer 85
DB 661 TCTGAATATATCC 672

RESULT 4
US-10-932-182A-4581
Sequence 4581, Application US/10932182A
Publication No. US20060046253A1
GENERAL INFORMATION:
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIRO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 030685-043
CURRENT APPLICATION NUMBER: US/10/932,182A
CURRENT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3

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; SEQ ID NO 4581.
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-4581

Alignment Scores:
Pred. No.: 9.14 Length: 771
Score: 70.50 Matches: 26
Percent Similarity: 35.5% Conservative: 18
Best Local Similarity: 21.0% Mismatches: 35
Query Match: 15.6% Indels: 45
DB: 7 Gaps: 4

US-10-071-645-2 (1-85) x US-10-932-182A-4581 (1-771)
Qy 7 TyrglyaspdluylsleuserProtyrglyaspdluylaspval----- 21
Db 301 TATGGCAATTCGAAATTCCTCCAGCTTATACGAACTGAAATCAACAGATACGATC 360
Qy 22 -----GlyGlnIlePheSerCyArgLeuGlnAptThraAsnAenPheNegIyala 38
Db 361 TTACAAAGGGGAGAGATTACCAACCCAGATGCTGACGCTGACAAATTTTTCGGTAA 420
Qy 39 GlyGlnAenlysaArgProlysbLeuGly-----GlnIleGlyArgSerlyArg 55
Db 421 CCGCAAGTGAAGAGAGAGCTGCTGCTGCTGAATTAATAGCTCAGACAAAGTAAAGCAGC 480
Qy 56 ValVal-----IleGluAsp 60
Db 481 TCGATTCGACGTATGAAAGATATCTTAATTTGACAGAGAAACAAATGTTACGAT 540
Qy 61 AsparGlyleAsp----- 64
Db 541 GATAGCTCTTCACTCACTCAACAAACGATGACAAATATGACAAATATGACATTAAT 600
Qy 65 -----AspValIleuIysAenMetThraAspIyalaProIleuValSerAenSerPro 81
Db 601 GAAACTTCCTCCGTTATTAGAAAATCCAGTAAAGCTCAGTATCATTAATATACCCCT 660
Qy 82 LysThrMetSer 85
Db 661 TCTGAAATATCC 672

RESULT 5
US-09-925-065A-600042
; Sequence 600042, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide, Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.335
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243, 096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250, 092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261, 766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289, 846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 600042
; LENGTH: 531
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-600042

```

```

Alignment Scores:
Pred. No.: 9.51 Length: 531
Score: 69.00 Matches: 17
Percent Similarity: 50.8% Conservative: 16
Best Local Similarity: 26.2% Mismatches: 22
Query Match: 15.2% Indels: 10
DB: 6 Gaps: 2

US-10-071-645-2 (1-85) x US-09-925-065A-600042 (1-531)
Qy 8 GlyAspdluylsleuserProtyrglyaspdluylaspvalGlyGlnIlePheSerCys 27
Db 232 GAGCAGAGGCCAAGAAATCCCAAGATGATGCGCTGCGTATCCAA----- 279
Qy 28 ArgLeuGlnAptThraAenPheNegIyalaGlyGlnAenlysaArgProIyaleu 47
Db 280 -----GATGGCATCAAGTCACAGCTCAGAGAGCAGCCTCCAGATTC 324
Qy 48 GlyGlnIleGlyArgSerlysaArgValIleIleGluAspAptThraAspValIleu 67
Db 325 GGGCAGATCAAGAAAGTTCCAGAGACACTTCTCAGAGAGACAAATCTAGAAATAGTT 384
Qy 68 LysAenMetThraAsp 72
Db 385 ---AATATGCTCGAA 396

RESULT 6
US-11-186-282-33
; Sequence 33, Application US/11186282
; Publication No. US2006025368A1
; GENERAL INFORMATION:
; APPLICANT: Adviays, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186, 282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33
; LENGTH: 2700
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is the optimized plasmid for Horse GHRH.
US-11-186-282-33

Alignment Scores:
Pred. No.: 86.2 Length: 2700
Score: 68.00 Matches: 18
Percent Similarity: 40.7% Conservative: 4
Best Local Similarity: 33.3% Mismatches: 20
Query Match: 15.0% Indels: 12
DB: 12 Gaps: 1

US-10-071-645-2 (1-85) x US-11-186-282-33 (1-2700)
Qy 15 TyrglyaspdluylaspvalGlyGlnIlePheSerCyArgLeuGlnAptThraAsn 34
Db 185 TATGGCAGAGGTTCTTCACCCGCTCCCATATTTGGGTGTCGCCCTCGCGGAGCGCA 244
Qy 35 PheNegIyalaGlyGlnAenlysaArgProIyals----- 46
Db 245 TTCCTGGGGGGCGGGCGGCTGCTCCCGCCGCTCGATTAAGAGCTCCGGGCGCGCGC 304
Qy 47 -----LeuGlyGlnIleGlyArgSerlysaArgVal 56
Db 305 GCCCAGAGCTACCCGGAGAGAGCGGAGCGCCCAAGCGGATC 346

RESULT 7
US-10-764-818A-17
; Sequence 17, Application US/10764818A
; Publication No. US20040204358A1
; GENERAL INFORMATION:

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; APPLICANT: ADVISYS
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CUL
; FILE REFERENCE: 108328.00170 - AVSI-0033
; CURRENT APPLICATION NUMBER: US/10/764,818A
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.1
; SEQ ID NO: 17
; LENGTH: 2710
; TYPE: DNA
; ORGANISM: artificial sequence
; OTHER INFORMATION: Codon optimized ("GHRH") sequence for mouse.
;
US-10-764-818A-17
Alignment Scores:
Pred. No.: 86.5 Length: 2710
Score: 68.00 Matches: 18
Percent Similarity: 40.7% Conservative: 4
Best Local Similarity: 33.3% Mismatches: 20
Query Match: 15.0% Indels: 12
DB: 7 Gaps: 1

US-10-071-645-2 (1-85) x US-10-764-818A-17 (1-2710)
QY 15 TyrGlyAspGlyGlyAspValGlyGlnIlePheSerCyArgLeuGlnAspThrAsnAsn 34
DB 219 TATGGCGACGGTTCCTCCACCCGTCGCGCATATTGGGTGTCCGCCCTCGCGCGGCGCGCA 278
QY 35 PhePheGlyAlaGlyGlnAsnIleArgProProlys----- 46
DB 279 TTCCTGGGGGCGCGGCGGTCTCCGCCGCTCGATAAAAGCTCCGGGCGCGGCGGCG 338
QY 47 -----LeuGlyGlnIleGlyArgSerIleArgVal 56
DB 339 GCCCAGAGCTACCCGGAGGAGCGGAGCGCCAGCGGATC 380

RESULT 8
US-10-764-818A-18
; Sequence 18, Application US/10764818A
; Publication No. US20040204358A1
; GENERAL INFORMATION:
; APPLICANT: ADVISYS
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CUL
; FILE REFERENCE: 108328.00170 - AVSI-0033
; CURRENT APPLICATION NUMBER: US/10/764,818A
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.1
; SEQ ID NO: 18
; LENGTH: 2713
; TYPE: DNA
; ORGANISM: artificial sequence
; OTHER INFORMATION: Codon optimized ("GHRH") sequence for rat.
;
US-10-764-818A-18
Alignment Scores:
Pred. No.: 86.6 Length: 2713
Score: 68.00 Matches: 18
Percent Similarity: 40.7% Conservative: 4
Best Local Similarity: 33.3% Mismatches: 20
Query Match: 15.0% Indels: 12
DB: 7 Gaps: 1

US-10-071-645-2 (1-85) x US-10-764-818A-18 (1-2713)
QY 15 TyrGlyAspGlyGlyAspValGlyGlnIlePheSerCyArgLeuGlnAspThrAsnAsn 34
DB 219 TATGGCGACGGTTCCTCCACCCGTCGCGCATATTGGGTGTCCGCCCTCGCGCGGCGCGCA 278
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QY 35 PhePheGlyAlaGlyGlnAsnIleArgProProlys----- 46
DB 279 TTCCTGGGGGCGCGGCGGTCTCCGCCGCTCGATAAAAGCTCCGGGCGCGGCGGCG 338
QY 47 -----LeuGlyGlnIleGlyArgSerIleArgVal 56
DB 339 GCCCAGAGCTACCCGGAGGAGCGGAGCGCCAGCGGATC 380

RESULT 9
US-10-764-818A-21
; Sequence 21, Application US/10764818A
; Publication No. US20040204358A1
; GENERAL INFORMATION:
; APPLICANT: ADVISYS
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CUL
; FILE REFERENCE: 108328.00170 - AVSI-0033
; CURRENT APPLICATION NUMBER: US/10/764,818A
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.1
; SEQ ID NO: 21
; LENGTH: 2713
; TYPE: DNA
; ORGANISM: artificial sequence
; OTHER INFORMATION: Codon optimized ("GHRH") sequence for chicken.
;
US-10-764-818A-21
Alignment Scores:
Pred. No.: 86.6 Length: 2713
Score: 68.00 Matches: 18
Percent Similarity: 40.7% Conservative: 4
Best Local Similarity: 33.3% Mismatches: 20
Query Match: 15.0% Indels: 12
DB: 7 Gaps: 1

US-10-071-645-2 (1-85) x US-10-764-818A-21 (1-2713)
QY 15 TyrGlyAspGlyGlyAspValGlyGlnIlePheSerCyArgLeuGlnAspThrAsnAsn 34
DB 219 TATGGCGACGGTTCCTCCACCCGTCGCGCATATTGGGTGTCCGCCCTCGCGCGGCGCGCA 278
QY 35 PhePheGlyAlaGlyGlnAsnIleArgProProlys----- 46
DB 279 TTCCTGGGGGCGCGGCGGTCTCCGCCGCTCGATAAAAGCTCCGGGCGCGGCGGCG 338
QY 47 -----LeuGlyGlnIleGlyArgSerIleArgVal 56
DB 339 GCCCAGAGCTACCCGGAGGAGCGGAGCGCCAGCGGATC 380

RESULT 10
US-10-764-818A-19
; Sequence 19, Application US/10764818A
; Publication No. US20040204358A1
; GENERAL INFORMATION:
; APPLICANT: ADVISYS
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CUL
; FILE REFERENCE: 108328.00170 - AVSI-0033
; CURRENT APPLICATION NUMBER: US/10/764,818A
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.1
; SEQ ID NO: 19
; LENGTH: 2716
; TYPE: DNA
; ORGANISM: artificial sequence
; OTHER INFORMATION: Codon optimized ("GHRH") sequence for bovine.
;
US-10-764-818A-19
Alignment Scores:
```

Pred. No.: 86.7 Length: 2716
 Score: 68.00 Matches: 18
 Percent Similarity: 40.7% Conservative: 20
 Best Local Similarity: 33.3% Mismatches: 40
 Query Match: 15.0% Indels: 12
 DB: 7 Gaps: 1

US-10-071-645-2 (1-85) x US-10-764-818A-19 (1-2716)

QY 15 TTTGTCGAGGCTTCTCCACCGCTGCGCATATTGGGTGTCGCCCTCGCGCGGCGCGCA 34
 DB 185 TATGGCAGCGGTCTCCACCGCTGCGCATATTGGGTGTCGCCCTCGCGCGGCGCGCA 244
 QY 35 PhepHeG1yAlaG1yGlnAmLysArgProProLys----- 46
 DB 245 TTCTGTGGGGCGCGGGCGGTCTCCGCCCGCTCGATAAAGGCTCCGGGGCGCGGCGG 304
 QY 47 -----LeuG1yGln1leG1yArgSerLysArgVal 56
 DB 305 GCCCAGAGCTACCGGAGAGCGGAGCGGCGCAACCGGATC 346

RESULT 11

US-10-764-818A-20
 ; Sequence 20 Application US/10764818A
 ; Publication No US20040204358A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ADVISYS
 ; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CUI
 ; FILE REFERENCE: 108328.00170 - AVSI-0033
 ; CURRENT APPLICATION NUMBER: US/10764,818A
 ; CURRENT FILING DATE: 2004-01-26
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 20
 ; LENGTH: 2716
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Tcodon optimized ("GHRH") sequence for ovine.

US-10-764-818A-20
 ; Sequence 20 Application US/10764818A
 ; Publication No US20040204358A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ADVISYS
 ; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CUI
 ; FILE REFERENCE: 108328.00170 - AVSI-0033
 ; CURRENT APPLICATION NUMBER: US/10764,818A
 ; CURRENT FILING DATE: 2004-01-26
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 20
 ; LENGTH: 2716
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Tcodon optimized ("GHRH") sequence for ovine.

Alignment Scores:
 Pred. No.: 86.7 Length: 2716
 Score: 68.00 Matches: 18
 Percent Similarity: 40.7% Conservative: 20
 Best Local Similarity: 33.3% Mismatches: 40
 Query Match: 15.0% Indels: 12
 DB: 7 Gaps: 1

US-10-071-645-2 (1-85) x US-10-764-818A-20 (1-2716)

QY 15 TTTGTCGAGGCTTCTCCACCGCTGCGCATATTGGGTGTCGCCCTCGCGCGGCGCGCA 34
 DB 185 TATGGCAGCGGTCTCCACCGCTGCGCATATTGGGTGTCGCCCTCGCGCGGCGCGCA 244
 QY 35 PhepHeG1yAlaG1yGlnAmLysArgProProLys----- 46
 DB 245 TTCTGTGGGGCGCGGGCGGTCTCCGCCCGCTCGATAAAGGCTCCGGGGCGCGGCGG 304
 QY 47 -----LeuG1yGln1leG1yArgSerLysArgVal 56
 DB 305 GCCCAGAGCTACCGGAGAGCGGAGCGGCGCAACCGGATC 346

RESULT 12

US-11-186-282-27
 ; Sequence 27 Application US/11186282
 ; Publication No. US2006025368A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ADVISYS, Inc.
 ; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
 ; FILE REFERENCE: 108328.000265 AVSI-0042
 ; CURRENT APPLICATION NUMBER: US/11186,282

;; CURRENT FILING DATE: 2005-07-21
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 27
 ; LENGTH: 2716
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: This is the codon optimized dog-GHRH expression plasmid.

US-11-186-282-27
 ; Sequence 27 Application US/11186282
 ; Publication No. US2006025368A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ADVISYS, Inc.
 ; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
 ; FILE REFERENCE: 108328.000265 AVSI-0042
 ; CURRENT APPLICATION NUMBER: US/11186,282
 ; CURRENT FILING DATE: 2005-07-21
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 28
 ; LENGTH: 2716
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: This is the codon optimized bovine-GHRH expression plasmid.

Alignment Scores:
 Pred. No.: 86.7 Length: 2716
 Score: 68.00 Matches: 18
 Percent Similarity: 40.7% Conservative: 20
 Best Local Similarity: 33.3% Mismatches: 40
 Query Match: 15.0% Indels: 12
 DB: 12 Gaps: 1

US-10-071-645-2 (1-85) x US-11-186-282-27 (1-2716)

QY 15 TTTGTCGAGGCTTCTCCACCGCTGCGCATATTGGGTGTCGCCCTCGCGCGGCGCGCA 34
 DB 185 TATGGCAGCGGTCTCCACCGCTGCGCATATTGGGTGTCGCCCTCGCGCGGCGCGCA 244
 QY 35 PhepHeG1yAlaG1yGlnAmLysArgProProLys----- 46
 DB 245 TTCTGTGGGGCGCGGGCGGTCTCCGCCCGCTCGATAAAGGCTCCGGGGCGCGGCGG 304
 QY 47 -----LeuG1yGln1leG1yArgSerLysArgVal 56
 DB 305 GCCCAGAGCTACCGGAGAGCGGAGCGGCGCAACCGGATC 346

RESULT 13

US-11-186-282-28
 ; Sequence 28 Application US/11186282
 ; Publication No. US2006025368A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ADVISYS, Inc.
 ; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
 ; FILE REFERENCE: 108328.000265 AVSI-0042
 ; CURRENT APPLICATION NUMBER: US/11186,282
 ; CURRENT FILING DATE: 2005-07-21
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 28
 ; LENGTH: 2716
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: This is the codon optimized bovine-GHRH expression plasmid.

US-11-186-282-28

Alignment Scores:
 Pred. No.: 86.7 Length: 2716
 Score: 68.00 Matches: 18
 Percent Similarity: 40.7% Conservative: 20
 Best Local Similarity: 33.3% Mismatches: 40
 Query Match: 15.0% Indels: 12
 DB: 12 Gaps: 1

US-10-071-645-2 (1-85) x US-11-186-282-28 (1-2716)

QY 15 TTTGTCGAGGCTTCTCCACCGCTGCGCATATTGGGTGTCGCCCTCGCGCGGCGCGCA 34
 DB 185 TATGGCAGCGGTCTCCACCGCTGCGCATATTGGGTGTCGCCCTCGCGCGGCGCGCA 244
 QY 35 PhepHeG1yAlaG1yGlnAmLysArgProProLys----- 46
 DB 245 TTCTGTGGGGCGCGGGCGGTCTCCGCCCGCTCGATAAAGGCTCCGGGGCGCGGCGG 304
 QY 47 -----LeuG1yGln1leG1yArgSerLysArgVal 56

Db 305 GCCCAGAGCTACCCGAGAGCGGAGCGCCAGCGGATC 346

RESULT 14

US-11-186-282-29

Sequence 29, Application US//11186282

Publication No. US20060025368A1

GENERAL INFORMATION:

APPLICANT: Advisys, Inc.

TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response

FILE REFERENCE: 106328.000265 AYSI-0042

CURRENT APPLICATION NUMBER: US//11/186,282

CURRENT FILING DATE: 2005-07-21

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn version 3.3

SEQ ID NO 29

LENGTH: 2716

TYPE: DNA

ORGANISM: artificial sequence

FEATURE:

OTHER INFORMATION: This is the codon optimized cat-GHRH expression plasmid.

US-11-186-282-29

Alignment Scores:

Pred. No.: 86.7 Length: 2716

Score: 68.00 Matches: 18

Percent Similarity: 40.7% Conservative: 4

Best Local Similarity: 33.3% Mismatches: 20

Query Match: 15.0% Indels: 12

DB: 12 Gaps: 1

US-10-071-645-2 (1-85) x US-11-186-282-29 (1-2716)

Qy 15 TyrGlyAaPglYgLYaSPValGlyGlnIlePheSerCyAArgLeuGlnAspThrAsnAsn 34

Db 185 TATGGCGACGGTTCCTCACCCTCCGCATATTGGGTCTCCGCCCTCGCGCGGCGCA 244

Qy 35 PhePheGlyAlaGlyGlnAsnIleSarProProlys----- 46

Db 245 TTCTGGGGGGCGGGCGGTCTCCGCCCTCGATAAAGGCTCCGGGGCGCGCGCG 304

Qy 47 -----LeuGlyGlnIleGlyAArgSerIleArgVal 56

Db 305 GCCCAGAGCTACCCGAGAGCGGAGCGCCAGCGGATC 346

RESULT 15

US-11-186-282-31

Sequence 31, Application US//11186282

Publication No. US20060025368A1

GENERAL INFORMATION:

APPLICANT: Advisys, Inc.

TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response

FILE REFERENCE: 106328.000265 AYSI-0042

CURRENT APPLICATION NUMBER: US//11/186,282

CURRENT FILING DATE: 2005-07-21

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn version 3.3

SEQ ID NO 31

LENGTH: 2716

TYPE: DNA

ORGANISM: artificial sequence

FEATURE:

OTHER INFORMATION: This is the codon optimized ovine-GHRH expression plasmid.

US-11-186-282-31

Alignment Scores:

Pred. No.: 86.7 Length: 2716

Score: 68.00 Matches: 18

Percent Similarity: 40.7% Conservative: 4

Best Local Similarity: 33.3% Mismatches: 20

Query Match: 15.0% Indels: 12

DB: 12 Gaps: 1

US-10-071-645-2 (1-85) x US-11-186-282-31 (1-2716)

Qy 15 TyrGlyAaPglYgLYaSPValGlyGlnIlePheSerCyAArgLeuGlnAspThrAsnAsn 34

Db 185 TATGGCGACGGTTCCTCACCCTCCGCATATTGGGTCTCCGCCCTCGCGCGGCGCA 244

Qy 35 PhePheGlyAlaGlyGlnAsnIleSarProProlys----- 46

Db 245 TTCTGGGGGGCGGGCGGTCTCCGCCCTCGATAAAGGCTCCGGGGCGCGCGCG 304

Qy 47 -----LeuGlyGlnIleGlyAArgSerIleArgVal 56

Db 305 GCCCAGAGCTACCCGAGAGCGGAGCGCCAGCGGATC 346

Search completed: March 9, 2006, 00:12:19

Job time : 327 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus.p2n model

Run on: March 8, 2006, 23:45:05 ; Search time 3028 Seconds

(without alignments)
1313.376 Million cell updates/sec

Title: US-10-071-645-2

Perfect score: 453

Sequence: 1 MMVLPYGPDEKLSPYGDCG.....VLKNTDKAPLVNSPKTWS 85

Scoring table:

BLOSUM62

Xgapop 10.0, Xgapext 0.5

Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 41078325 seqs, 2339541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frames.p2n.model -DEV=xlh

-Q=abs/ABSWEB.spool/US10071645/runat.08032006.115123.4660/apd_query.fasta_1

-DB=EST -QFMT=fastap -SUFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0

-UNITS=bits -START=1 -END=1 -MATRIX=blosome62 -TRANS=human40.cdi -LIST=45

-DOCALLIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL

-DOCALLIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL

-USER=US10071645.00CN.1.1.5315.0runat.08032006.115123.4660 -NCPU=6 -ICPU=3

-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120

-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7

-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hic:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gse81:*

10: gb_gse82:*

11: gb_gse83:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	413	91.2	449	1	AM162736
C 2	413	91.2	503	1	AM162736
C 3	413	91.2	579	7	CO706092
C 4	413	91.2	595	5	BU633970
C 5	413	91.2	654	8	DN989828
C 6	413	91.2	676	5	BQ771726
C 7	413	91.2	819	3	BI553632

C 8	413	91.2	981	7	CN801823
C 9	412	90.3	619	8	DN541682
C 10	412	90.3	621	8	DN542741
C 11	412	90.3	663	7	CN787570
C 12	406	89.6	548	1	AI683522
C 13	405	89.4	428	1	AM027389
C 14	405	89.4	459	1	AM027920
C 15	396	87.4	429	8	CX122497
C 16	369	81.5	520	1	AM162846
C 17	295.5	65.2	528	7	CO692011
C 18	295.5	65.2	708	8	CX846142
C 19	295.5	65.2	737	8	CX840681
C 20	295.5	65.2	761	8	CX822416
C 21	295.5	65.2	764	8	CX846426
C 22	295.5	65.2	799	8	CX825823
C 23	295.5	65.2	801	8	CX824373
C 24	295.5	65.2	812	8	CX856179
C 25	295.5	65.2	832	8	CX829330
C 26	295.5	65.2	842	8	CX829481
C 27	295.5	65.2	873	8	CX823227
C 28	291.5	64.3	835	6	CB555981
C 29	291.5	64.3	917	5	BU904054
C 30	289.5	64.0	287	10	CE790150
C 31	288.5	63.7	780	5	BX853591
C 32	277.5	61.3	1140	3	BO276281
C 33	277.5	61.3	546	3	BA772750
C 34	277.5	61.3	560	7	CO351424
C 35	277.5	61.3	782	7	CO813545
C 36	277.5	61.3	840	7	CK398028
C 37	277.5	61.3	868	7	CN841328
C 38	273.5	60.4	344	7	CN217279
C 39	273.5	60.4	854	7	CN843529
C 40	273.5	60.4	864	7	CK017491
C 41	273.5	60.4	870	7	CN331629
C 42	273.5	60.4	871	7	CN502825
C 43	270.5	59.7	541	3	BM496054
C 44	270.5	59.7	464	5	BU120469
C 45	270.5	59.7	661	7	CK688129

ALIGNMENTS

RESULT 1
AM162736/c
LOCUS
DEFINITION
aust707.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone
IMAGE:2783293.3, similar to TR:Q922N6 Q922N6 CAM-KII INHIBITORY
PROTEIN, mRNA sequence.

ACCESSION
AM162736.1 GI:6301769

VERSION
EST

KEYWORDS
Homo sapiens (human)

SOURCE
Homo sapiens

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

REFERENCE
1 (bases 1 to 449)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisell, G., Jost, S.,
Kritman, D., Kuba, T., Lacy, M., Le, N., Lennon, G., Marz, M.,
Martin, J., Moore, B., Scheinberg, R., Steptoe, M., Tan, F.,
Wheising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.

TITLE
JOURNAL
Unpublished (1997)

COMMENT
Contact: Wilson RK

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LNC, contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40UP from Gldco

High quality sequence stop: 404.

RESULT 3
 COT06092/c 579 bp mRNA linear EST 26-JUL-2004
 LOCUS DG32-47k17 DG32-11ver Canis familiaris cDNA 3', mRNA sequence.
 DEFINITION COT06092
 ACCESSION COT06092.1 GI:50654793
 VERSION EST
 KEYWORDS Canis familiaris (dog)
 SOURCE Canis familiaris
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE
 1 (bases 1 to 579)
 Schlueter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H., Henrich, J., and Loebbert, R.
 Dog arrayTAG cDNA clone collection
 Unpublished (2004)
 CONTACT: Thomas Schlueter
 LION Bioscience AG
 Waldhoferstrasse 98, D-69123 Heidelberg, Germany
 Tel: +49 6221 4038 150
 Fax: +49 6221 4038 290
 Email: Thomas.Schlueter@lionbioscience.com.

FEATURES
 source 1
 579
 location/Qualifiers
 /organism="Canis familiaris"
 /mol_type="mRNA"
 /strain="Beagle"
 /db_xref="taxon:9615"
 /tissue_type="Liver"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1ib="DG32-11ver"
 /note="Organ: liver; Vector: Dog pBluescript LION"

ORIGIN
 Alignment Scores:
 Pred. No.: 1.33e-45 Length: 579
 Score: 413.00 Matches: 84
 Percent Similarity: 96.6% Conservative: 0
 Best Local Similarity: 96.6% Mismatches: 1
 Query Match: 91.2% Indels: 2
 DB: 7 Gaps: 0

US-10-071-645-2 (1-85) x COT06092 (1-579)

QY 1 MetTTPGluValLeuProTyrGlyAspGluIuylsLeuSerProTyrGlyAspGlyIuylasp 20
 Db 560 ATGTGGAGGGTGGCTGCTGCTGACGAGAGAGCTGAGCCCTTACGGGACGCGCGGAC 501

QY 21 ValGlyGlnIlePheSerCysArgLeuGlnAspPheAspPhePheGlyValAGlyGln 40
 Db 500 GTGGGCCAGATCTTCTCTGCGCTGACGAGACCAACTTCTTGGCGCGCGGACG 441

QY 41 AmlYsArgProPheIuylsLeuGlyGlnIleGlyAspSerIuylsValValIleGluAap 60
 Db 440 AACAAAGCCGCCGCCCAAGCTGGGCGAGATCGGCGGAGCGAGGAGTGTATTGAGAGT 381

QY 61 AapArgIleAspAspValLeuIuylsAspMetThrAspIuylsAlaPro-LeuValSerAsp 80
 Db 380 GATGAGATTGATGACGCTGCAAAATATGACAGACAGGACCTCTGCTGCTTAACTC 321

QY 80 T-ProlySerMetSer 85
 Db 320 CCCCAAGACATGAGT 304

RESULT 4
 BU633970/c 595 bp mRNA linear EST 23-SEP-2002
 LOCUS UI-H-FL1-bgw-c-22-0-UI .s1 NCI CGAP FL1 Homo sapiens cDNA clone
 DEFINITION UI-H-FL1-bgw-c-22-0-UI 3', mRNA sequence.
 ACCESSION BU633970
 VERSION BU633970.1 GI:23301225

KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 1 (bases 1 to 595)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strauberg, Ph.D.
 Email: rgs@biotech.nih.gov
 Tissue Procurement: James Martin
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA library arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA sequence: 1-109, POLY_ASimple_repeat (matched complement) 126-167, >(GGA)n(Simple_repeat (matched complement)
 Seq primer: M13 FORWARD
 Polya-ies.

FEATURES
 source 1
 595
 location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FL1-bgw-c-22-0-UI"
 /tissue_type="Cell lines"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_1ib="NCI CGAP FL1"
 /note="Organ: Chondrosarcoma; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FL1 is a normalized cDNA library derived from a pool of mRNA obtained from 4 cell lines from grade III chondrosarcoma tissues. The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The cell lines were provided by Dr. James Martin from the University of Iowa. TRG Tissue: Human Chondrosarcoma Grade 3 cell line mix TRG_Lib-UI-H-FL1 TRG_SEQ-GAGTGGTGC"

ORIGIN
 Alignment Scores:
 Pred. No.: 1.37e-45 Length: 595
 Score: 413.00 Matches: 84
 Percent Similarity: 96.6% Conservative: 0
 Best Local Similarity: 96.6% Mismatches: 1
 Query Match: 91.2% Indels: 2
 DB: 5 Gaps: 0

US-10-071-645-2 (1-85) x BU633970 (1-595)

QY 1 MetTTPGluValLeuProTyrGlyAspGluIuylsLeuSerProTyrGlyAspGlyIuylasp 20
 Db 551 ATGTGGAGGGTGGCTGCTGCTGACGAGAGAGCTGAGCCCTTACGGGACGCGCGGAC 492

QY 21 ValGlyGlnIlePheSerCysArgLeuGlnAspThrAspAspPheGlyValAGlyGln 40
 Db 491 GTGGGCCAGATCTTCTCTGCGCTGACGAGACCAACTTCTTGGCGCGCGGACG 432

QY 41 AsnlysaRpproProlysleuGlyglnIleGlyAArgSerIyAArgValIleGluasp 60
 Db 431 AACAGCGCGCCGCCGCGAGTCCAGATCGAGCGAGCGAGCGAGTGTATTGAGAT 372
 QY 61 AsparG11eAspAspValIleuLysaRnMetThraAspYsAlaPro-LeuValSerAaSe 80
 Db 371 GATGAGATTGATGACGCTGCTGAAAATATGACGACGACGACCTCTGCTGCTAACTC 312
 QY 80 r-ProlyerThMetSer 85
 Db 311 CCCCAAGACAAATGAGT 295

RESULT 5
 LOCUS DN989828 654 bp mRNA linear EST 17-MAY-2005
 DEFINITION TC113435 Human adult whole brain, large insert, pcwv expression library Homo sapiens cDNA clone TC113435 5' similar to Homo sapiens calcium/calmodulin-dependent protein kinase II (CamK11A1pha), mRNA sequence.
 DN989828
 ACCESSION DN989828.1 GI:66249659
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 654)
 Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L., Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Jay,G. and He,W.
 High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts
 Unpublished (2005)
 CONTACT: Kovacs, KP
 High Throughput cDNA Cloning
 Origene Technologies, Inc. (www.origene.com)
 6 Taft Court, Suite 100, Rockville, MD 20850, USA
 Tel: 301 340 3188
 Fax: 301 340 8606
 Email: cDNA@origene.com
 This EST submission is part of an on-going human full-length cloning project at Origene Technologies, Inc.
 Please contact Origene for access.
 Origene Technologies, Inc.
 6 Taft Ct. Suite 100
 Rockville, MD 20850
 Tel: (301) 340-3188
 http://www.origene.com
 Seq primer: PCWV6 5prime forward vector primer, Origene Technologies Inc.

FEATURES
 source
 1..654
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="TC113435"
 /tissue_type="Whole brain"
 /clone_lib="Human adult whole brain, large insert, pcwv expression library"
 /note="Organ: Brain; Vector: PCWV6-XL5; Site 1: EcoRI; Site 2: XhoI/SalI compatible end ligatio; Oligo-dt primed reverse transcription optimized for large and GC rich mRNA transcripts, cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected for end sequence verification of full-length genes"

ORIGIN
 Alignment Scores:
 Pred. No.: 1,54e-45 Length: 654
 Score: 413.00 Matches: 84
 Percent Similarity: 96.6% Conservative: 0

Best Local Similarity: 96.6%
 Query Match: 81.2%
 DB: 8 Gaps: 2
 US-10-071-645-2 (1-85) x DN989828 (1-654)

QY 1 MetTTPG1uValleuProTyGlyAspGluYsleuSerProTyGlyAspGlyasp 20
 Db 68 ATGTGAGAGTGTCTGCTTACGCGACGAGGAGCTGAGCCCTTACGACGCGGAC 127
 QY 21 ValGlyGlnIlePheSerCyAArgleuGlnAspThraAaRnBheG1yAlaGlyGln 40
 Db 128 GTGGGCGAGATCTTCTCTGCGCGCGACGACACCAACTTCTTGGCGCGCGGACG 187
 QY 41 AsnlysaRpproProlysleuGlyglnIleGlyAArgSerIyAArgValIleGluasp 60
 Db 188 AACAGCGCGCCGCCGAGTCCAGATCGAGCGAGCGAGCGAGGCTGTATTGAGAT 247
 QY 61 AsparG11eAspAspValIleuLysaRnMetThraAspYsAlaPro-LeuValSerAaSe 80
 Db 248 GATAGGATTGATGACGCTGCTGAAAATATGACGACGACGACCTCTGCTGCTAACTC 307
 QY 80 r-ProlyerThMetSer 85
 Db 308 CCCCAAGACAAATGAGT 324

RESULT 6
 LOCUS BQ771726/c 676 bp mRNA linear EST 26-JUL-2002
 DEFINITION U1-H-E21-bbj-h-10-0-UI.61 NCI CGAP Ch2 Homo sapiens cDNA clone U1-H-E21-bbj-h-10-0-UI 3', mRNA sequence.
 BQ771726
 ACCESSION BQ771726.1 GI:21980202
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 676)
 NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Steven Gitelils/ Rush Presbyterian, Dept. of Orthopedics
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA sequence: 35-76, >(GGA)nSimple repeat (matched complement) 469-512, >GC richlow complexity (matched complement) 513-595, >(CGG)nSimple repeat
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES
 source
 1..676
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="U1-H-E21-bbj-h-10-0-UI"
 /tissue_type="Chondrosarcoma Grade II"
 /dev stage="Adult"
 /lab host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP Ch2"
 /note="Organ: Left pelvis; Vector: pT771-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP Ch2 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma Grade II. The library

was constructed according to Ronaldo, Lennon and Soares, Genome Research 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTV73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is TGAACAGCT.

TAG TISSUE=grade-2-chondrosarcoma
TAG LIB=UI-H-E21
TAG SEQ=ATCTAATATG

ORIGIN

Alignment Scores:
Pred. No.: 1,61e-45 Length: 676
Score: 413.00 Matches: 84
Percent Similarity: 96.6% Conservative: 0
Best Local Similarity: 96.6% Mismatches: 1
Query Match: 91.2% Indels: 2
DB: 5 Gaps: 0

US-10-071-645-2 (1-85) x BQ771726 (1-676)

QY 1 MetTTPGluValLeuProTgLYAspGluValLeuSerProTYRGlyAspGlyValAsp 20
DB 460 ATGTGCGAGAGTCTGCTCCCTACGCGACGACGAACTGAGCCCTACGCGCGCGCGAC 401
QY 21 ValGlyGlnIlePheSerCyArgLeuGlnAspThrAsnAspPheGlyValGlyGln 40
DB 400 GTGGGCGCAAGTCTTCTCCGCGCGCTGAGACACACCAACATCTTCGCGCGCGCGACG 341
QY 41 AsnLYAspProProLYLeuGlyGlnIleGlyAspSerLYAspValValIleGluAsp 60
DB 340 AACCAAGCG 281
QY 61 AspArgIleAspAspValLeuLYAspMetThrAspLYAspValAspPro-LeuValSerAsn 80
DB 280 GATGAGATTGATGACGTGTAATAATATGACCGACGACGACCTCTGCTGCTTAATC 221
QY 80 T-ProLYThrMetSer 85
DB 220 CCCCAAGACATGACT 204

RESULT 7
BI553632 819 bp mRNA linear EST 05-SEP-2001
LOCUS 603190553P1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5262036 5',
DEFINITION mRNA sequence.
ACCESSION BI553632
VERSION BI553632.1 GI:15440944
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo
1 (bases 1 to 819)
NIH-MGC http://mgi.mgi.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgsb@remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki
Toshiyuki and Piero Carninci (RIKEN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/MLM at:
http://image.llnl.gov
Plate: LHM11660 row: 1 column: 13

High quality sequence STOP: 784.

FEATURES
source Location/Qualifiers
1..819

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5262036"
/issue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
(gtag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTNN-3', size-selected for average
insert size 2.5 kb and normalized to R0T 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC library."

ORIGIN

Alignment Scores:
Pred. No.: 2.04e-45 Length: 819
Score: 413.00 Matches: 84
Percent Similarity: 96.6% Conservative: 0
Best Local Similarity: 96.6% Mismatches: 1
Query Match: 91.2% Indels: 2
DB: 5 Gaps: 0

US-10-071-645-2 (1-85) x BI553632 (1-819)

QY 1 MetTTPGluValLeuProTgLYAspGluValLeuSerProTYRGlyAspGlyValAsp 20
DB 17 ATGTGCGAGAGTCTGCTCCCTACGCGACGACGAACTGAGCCCTACGCGCGCGCGAC 76
QY 21 ValGlyGlnIlePheSerCyArgLeuGlnAspThrAsnAspPheGlyValGlyGln 40
DB 77 GTGGGCGCAAGTCTTCTCCGCGCGCTGAGACACCAACATCTTCGCGCGCGCGACG 136
QY 41 AsnLYAspProProLYLeuGlyGlnIleGlyAspSerLYAspValValIleGluAsp 60
DB 137 AACCAAGCG 196
QY 61 AspArgIleAspAspValLeuLYAspMetThrAspLYAspValAspPro-LeuValSerAsn 80
DB 197 GATGAGATTGATGACGTGTAATAATATGACCGACGACGACCTCTGCTGCTTAATC 256
QY 80 T-ProLYThrMetSer 85
DB 257 CCCCAAGACATGACT 273

RESULT 8
CN801823 981 bp mRNA linear EST 26-MAY-2004
LOCUS ILUMWGEN_MGC_37102 Katze_WMR Macaca mulatta cDNA clone
IBIOW:15513 5', similar to bases 200 to 940 highly similar to human
CARKIN1Alp1a (Hs.197922), mRNA sequence.
ACCESSION CN801823
VERSION CN801823.1 GI:47697799
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecoidea; Macaca.
1 (bases 1 to 981)
Magnes, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B.,
Prohl, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
Iadonato, S.P.
Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human
Genome Biol. 6 (7), R60 (2005)

PUBMED
COMMENT 15998449
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.05.13. 739 Q20 bases.
PCR Primers
FORWARD: CCTCACTTAAGGAAACAAA
BACKWARD: CACTATAGGCGCATTTGGTA
Insert Length: 981 Std Error: 0.00
Plate: CL000291 row: B column: 02
Seq primer: CCTCACTTAAGGAAACAAA
POLYA=yes.

FEATURES
source Location/Qualifiers
1..981
/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IBITM:15513"
/sex="female"
/dev_stage="adult"
/lab_host="E. coli SOLR"
/clone_1ib="Katze, MBR"
/note="Organ: brain; Vector: Uni-ZAP XR; Site_1: EcoR I;
Site_2: Xho I; Created from Stratagene ZAP-CDNA Synthesis
kit (catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"

ORIGIN

Alignment Scores:

Pred. No.: 2.55e-45 Length: 981
Score: 413.00 Matches: 84
Percent Similarity: 96.6% Conservative: 0
Best Local Similarity: 96.6% Mismatches: 1
Query Match: 91.2% Indels: 2
DB: 7 Gaps: 0

US-10-071-645-2 (1-85) x CN801823 (1-981)

QY 1 MetTTPGluValLeuProTyrglyAspGluysleuSerProTyrglyAspGlyValAsp 20
DB 42 ATCTCGAGAGTGTCTCTCCCTACGCGCAGCAAGAGCTGAGCCCTACGCGCAGCGCGCGAC 101
QY 21 ValGlyGlnIlePheSerCysArgLeuGlnAspThrAsnAsnPhenheGlyValGlyGln 40
DB 102 GTGGGCGAGATCTTCTCTCTCGCGCAGACACCAACTTCTTGGGCGCGCGCGAG 161
QY 41 AsnlyAspPropProlySleuGlyGlnIleGlyArgSerIlyAspValValIleGluAsp 60
DB 162 AACCAAGCGCGCCGCCCAAGCTGGCCCAATCGCTCGAGCAAGCGGATGTATTGAAGAT 221
QY 61 AspArgIleAspAspValIleuysAsnMetThrAspIlyAspPro-IeuValSerAsnse 80
DB 222 GATAGATTGATGAGCTGTAATAATATGACCAAGGACACTCTCTGTCTTAATCT 281
QY 80 r-ProlysthrMetSer 85
DB 282 CCCCAAGACATGAGT 298

RESULT 9
DNS41682/ 619 bp mRNA linear EST 11-MAR-2005
LOCUS DNS41682
DEFINITION 1390289 MARC 7BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION DNS41682
VERSION DNS41682.1 GI:60998793
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

REFERENCE
AUTHORS 1 (bases 1 to 619)
Smith,T.P.L., Roberts,A.J., Echterkamp,S.E., Chitko-McKown,C.G.,
Wray,J.E. and Keele,J.W.
TITLE A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL Unpublished (2003)
CONTACT: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
plate: RLK8071 row: J column: 20
Seq primer: TAGAGGACAGCTGAGG.

FEATURES
source Location/Qualifiers
1..619
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_1ib="MARC 7BOV"
/note="Vector: pCDNA3.1; Site_1: EcoRI; Site_2: NotI;
Library made with RNA pooled from multiple tissues
including ovary, hindbrain, uterus, and day-30 whole
embryos."

ORIGIN

Alignment Scores:

Pred. No.: 1.97e-45 Length: 619
Score: 412.00 Matches: 83
Percent Similarity: 96.6% Conservative: 1
Best Local Similarity: 95.4% Mismatches: 2
Query Match: 90.9% Indels: 2
DB: 8 Gaps: 0

US-10-071-645-2 (1-85) x DNS41682 (1-619)

QY 1 MetTTPGluValLeuProTyrglyAspGluysleuSerProTyrglyAspGlyValAsp 20
DB 442 ATCTCGAGAGTGTCTCTCCCTACGCGCAGCAAGAGCTGAGCCCTACGCGCAGCGCGAC 383
QY 21 ValGlyGlnIlePheSerCysArgLeuGlnAspThrAsnAsnPhenheGlyValGlyGln 40
DB 382 GTGGGCGAGATCTTCTCTCTCGCGCAGACACCAACTTCTTGGGCGCGCGCGAG 323
QY 41 AsnlyAspPropProlySleuGlyGlnIleGlyArgSerIlyAspValValIleGluAsp 60
DB 322 AACCAAGCGCGCCGCCCAAGCTGGCCCAATCGCTCGAGCAAGCGGATGTATTGAAGAT 263
QY 61 AspArgIleAspAspValIleuysAsnMetThrAspIlyAspPro-IeuValSerAsnse 80
DB 262 GATAGATTGATGAGCTGTAATAATATGACCAAGGACACTCTCTGTCTTAATCT 203
QY 80 r-ProlysthrMetSer 85
DB 202 CCCCAAGACATGAGT 186

RESULT 10
DNS42741 661 bp mRNA linear EST 11-MAR-2005
LOCUS DNS42741
DEFINITION 1391521 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION DNS42741
VERSION DNS42741.1 GI:61001043
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 661)
AUTHORS Smith,T.P.L., Roberts,A.J., Echtenkamp,S.E., Chitko-McKown,C.G.,
Wray,J.E. and Keele,J.W.
TITLE A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Plate: RIK8071 row: J column: 20
Seq primer: GTAATACACTCCTACTATAGG.
Location/Qualifiers
1..661
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 7B0V"
/note="Vector: pCDNA3.1, Site 1: EcoRI; Site 2: NotI;
library made with RNA pooled from multiple tissues
including ovary, hindbrain, uterus, and day-30 whole
embryos."

ORIGIN
Alignment Scores:
Pred. No.: 2,14e-45 Length: 661
Score: 412.00 Matches: 83
Percent Similarity: 96.6% Conservative: 1
Best Local Similarity: 95.4% Mismatches: 1
Query Match: 90.9% Indels: 2
DB: 8 Gaps: 0

US-10-071-645-2 (1-85) x DNS42741 (1-661)

QY 1 MetTpglualleupProTyrGlyAspGluysleuSerProTyrGlyAspGlyGlyAsp 20
Db 220 ATGTGCGAGGTGCTGCTGCGCCACGACGACGAGCTGAGCCCTTACGCGGCGGCGAC 279
QY 21 ValGlyGlnIlePheSerCysArgLeuGlnAspThrAsnAspPheGlyValGlyGln 40
Db 280 GTGGGCGGAGTCTTCTCTGCGCGCTGCGAGGACCAACTTCTTGGCGCGGCGGCG 339
QY 41 AsnlysaTgProProlysleuGlyGlnIleGlyArgSerIysArgValIleGluAsp 60
Db 340 AACCAAGCGCGCGCCCAAGCTGGGCGCAATCGCTGAGCAAGCGGCTTATTGAAAT 399
QY 61 AsparGlleasparValIleuysAsnMetThrAspIysAlaPro-LeuValSerAsn 80
Db 400 GATGAGATTGATGACCTGCTGAAAATATGACAGACAGGCACTCTGAGTCTTAACTC 459
QY 80 r-ProlyserThrMetSer 85
Db 460 CCCCAAGACATGAGT 476

RESULT 11
CN787570 663 bp mRNA linear EST 26-MAY-2004
LOCUS 4121731 BARC 8BOV Bos taurus cDNA clone 8BOV_32C12 5', mRNA
DEFINITION Sequence.
ACCESSION CN787570
VERSION CN787570.1 GI:47683550
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 663)
AUTHORS Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassel,C.P. and
Metukumillai,L.K.
TITLE Construction and Analysis of a cDNA Library Generated From
JOURNAL Intestinal Muscle and Epithelial Tissues of Holstein Cattle
COMMENT Unpublished (2004)
Contact: Richard G. Baumann
Bovine Functional Genomics Lab
ANRI
BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
Tel: 3015048604
Fax: 3015048744
Email: rbaumann@nri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim alt '-' -trim fastavector identified by
cross match using options -mismatch 12 -mismatch 12
Plate: 32 row: C column: 12
Seq primer: CCTATTGCGGACACTATAGAC
High quality sequence stop: 663.
Location/Qualifiers
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/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone_lib="8BOV_32C12"
/sex="Female"
/tissue_type="Epithelial, Muscle"
/dev_stage="Lactating, Neonatal"
/lab_host="DH10B Tona"
/clone_lib="BARC 8BOV"
/note="Organ: Intestine; Vector: PCWVSPORT6.1; Site 1:
NotI; Site 2: EcoRI; Normalized cow cDNA intestinal
library in pCMVSPORT6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 lactating, proximal duodenum,
jejunum, distal ileum, colon, 1/5 Neonatal, proximal
duodenum, jejunum, distal ileum"

ORIGIN
Alignment Scores:
Pred. No.: 2,15e-45 Length: 663
Score: 412.00 Matches: 83
Percent Similarity: 96.6% Conservative: 1
Best Local Similarity: 95.4% Mismatches: 1
Query Match: 90.9% Indels: 2
DB: 7 Gaps: 0

US-10-071-645-2 (1-85) x CN787570 (1-663)

QY 1 MetTpglualleupProTyrGlyAspGluysleuSerProTyrGlyAspGlyGlyAsp 20
Db 251 ATGTGCGAGGTGCTGCTGCGCCACGACGACGAGCTGAGCCCTTACGCGGCGGCGAC 310
QY 21 ValGlyGlnIlePheSerCysArgLeuGlnAspThrAsnAspPheGlyValGlyGln 40
Db 311 GTGGGCGGAGTCTTCTCTGCGCGCTGCGAGGACCAACTTCTTGGCGCGGCGGCG 370
QY 41 AsnlysaTgProProlysleuGlyGlnIleGlyArgSerIysArgValIleGluAsp 60
Db 371 AACCAAGCGCGCGCCCAAGCTGGGCGCAATCGCTGAGCAAGCGGCTTATTGAAAT 430
QY 61 AsparGlleasparValIleuysAsnMetThrAspIysAlaPro-LeuValSerAsn 80
Db 431 GATGAGATTGATGACGCTGAAAATATGACAGACAGGCACTCTGAGTCTTAACTC 490
QY 80 r-ProlyserThrMetSer 85
Db 491 CCCCAAGACATGAGT 507

RESULT 12
A0683522 548 bp mRNA linear EST 29-JUN-2004
LOCUS A0683522

DEFINITION AU683522 CSORAN04 Sus scrofa cDNA clone C0001802_F08, mRNA
SEQUENCE
ACCESSION AU683522
VERSION AU683522.1 GI:49416112
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
Sus.
REFERENCE 1 (bases 1 to 548)
Anderson, S.I., Filleyson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
JOURNAL Contact: Anderson SI
COMMENT Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -mnscore 20
and -mismatch 12 options. Vector: pBluescriptII (KS+). R. Site1: EcoRI
R. Site2: NotI 5' Seg Primer M13P Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS. www.arkgenomics.org.
FEATURES
source
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/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001802_F08"
/tissue_type="uterus"
/clone_lib="CSORAN04"
/note="vector: pBluescriptII (KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."
ORIGIN
Alignment Scores:
Pred. No.: 1,11e-44 Length: 548
Score: 406.00 Matches: 83
Percent Similarity: 95.4% Conservative: 0
Best Local Similarity: 95.4% Mismatches: 2
Query Match: 89.6% Indels: 2
DB: 1 Gaps: 0
US-10-071-645-2 (1-85) x AU683522 (1-548)
QY 1 MetTTPGIVaIIeuprOTyTgIYAaPgluYsLeuSerProTyTgIYAaPglYgIYAaP 20
Db 12 ATGTGCGAGGCTGCTGCTACGCGACGACGAGAGCTGATGCTCCACGCGGAGCGGCGGAC 71
QY 21 ValGIGInIlePheSerCySaRgLeuGInaPThraSnaSnphePheGlyAlaGlyGIn 40
Db 72 GTGGGCGCAGATCTTCTCTGCGCTGCGACGACGACCAATACCTCTTGGCGCGGCGACG 131
QY 41 AenLYsaRgPProPoyLYsLeuGInIleGlyARgSerLYsaRgValIleGluAaP 60
Db 132 AACCAAGCGCGCGCGCAAGCTGGGCGAGTGGCGGAGGAGGAGGCTTATTGAAGAT 191
QY 61 AsPaRgIleAsPaRValleuLYsaSnaMeThraPlySaLaPro-LeuValSerAaSe 80
Db 192 GATGAGATATATACGCTGCAAAAATATGACAGACAGGACCTCCCGGTGTAACTC 251
QY 80 T-ProLYeThMeSer 85
Db 252 CCCCAAGACATAGT 268
RESULT 13
AM027920/c 428 bp mRNA linear EST 30-JUN-2005
LOCUS AM027920/c
DEFINITION AM027920 KN-252-lymph, Bos indicus Bos indicus cDNA clone

ACCESSION C0007392f14 3', mRNA sequence.
VERSION AM027920
KEYWORDS AM027920.1 GI:68426991
SOURCE EST.
ORGANISM Bos indicus (Bos taurus indicus)
Bos indicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 428)
Anderson, S.I., Taylor, R., Talbot, R., Speed, D., Law, A.S.,
Humphrey, S., Hanotte, O., Mwaka, J. and Archibald, A.L.
Development of cDNA and EST resources for studying host responses
to trypanosome infection in cattle
Unpublished (2005)
JOURNAL Contact: Anderson SI
COMMENT Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM.
FEATURES
source
1..428
/organism="Bos indicus"
/mol_type="mRNA"
/db_xref="taxon:9915"
/clone="C0007392f14"
/tissue_type="lymph node"
/clone_lib="KN-252-lymph, Bos indicus"
/note="Breed: Boran"
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Alignment Scores:
Pred. No.: 1,12e-44 Length: 428
Score: 405.00 Matches: 81
Percent Similarity: 97.6% Conservative: 1
Best Local Similarity: 96.4% Mismatches: 0
Query Match: 89.4% Indels: 2
DB: 1 Gaps: 0
US-10-071-645-2 (1-85) x AM027920 (1-428)
QY 4 ValLeuProTYrGIYAaPgluYsLeuSerProTYrGIYAaPglYgIYAaPValGIn 23
Db 427 GTCTGTCCCTTCCGCGCGAGAGCTGAGCCCTTACGCGCGCGCGCGCGCGCGCGCAG 368
QY 24 IlePheSerCySaRgLeuGInaPThraSnaSnphePheGlyAlaGlyGInaSnLYsaRg 43
Db 367 GTCTTCTCTGCGCGCTGCGACGACCAAACTTTTTCGCGCGCGCGCGCGCGCGCGCAG 308
QY 44 ProProLYsLeuGInIleGlyARgSerLYsaRgValIleGluAaPAsPaRgIle 63
Db 307 CCCGCCAAGCTGGCGCAAAATCGGTCCGAGCAAGCGGCTGTATTGAAGATGATGATGATT 248
QY 64 AsPaRValleuLYsaSnaMeThraPlySaLaPro-LeuValSerAaSer-ProLYST 83
Db 247 GATGAGTGTCTGAAAAATATGACAGACAGGACCTCTGTGTAACTCCGCCAAGA 168
QY 83 hrMeSer 85
Db 187 CATGAGT 180
RESULT 14
AM027389 429 bp mRNA linear EST 30-JUN-2005
LOCUS AM027389
DEFINITION C0007392f14 5', mRNA sequence.
ACCESSION AM027389.1 GI:68426358
KEYWORDS EST.
ORGANISM Bos indicus (Bos taurus indicus)
Bos indicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 429)
AUTHORS Anderson, S.I., Taylor, R., Talbot, R., Speed, D., Law, A.S.,
Humphray, S., Hancock, O., Warkay, J., and Archibald, A.L.
TITLE Development of cDNA and EST resources for studying host responses
to trypanosome infection in cattle
JOURNAL Unpublished (2005)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM.
Location/Qualifiers
source 1..429
/organism="Bos indicus"
/mol_type="mRNA"
/db_xref="taxon:9915"
/clone="C0007392f14"
/tissue_type="lymph node"
/clone_lib="KN-252-lymph, Bos indicus"
/note="Breed: Boran"

ORIGIN
Alignment Scores:
Pred. No.: 1.12e-44 Length: 429
Score: 405.00 Matches: 81
Percent Similarity: 97.6% Conservative: 1
Best Local Similarity: 96.4% Mismatches: 0
Query Match: 89.4% Indels: 2
DB: 1 Gaps: 0
US-10-071-645-2 (1-85) x AN027389 (1-429)

QY 4 ValLeuProTyrGlyValAspGluValSerProTyrGlyValAspValGlyGln 23
Db 2 GTGCTGCCCTTACGCGACAGAGAGTGGCCCTTACGCGAGCGCGCGAGCGGCGCG 61
QY 24 IlePheSerCysArgLeuGlnAspThrAsnAsnPhePheGlyValGlyGlnAsnValArg 43
Db 62 GTCTTCTCCGCGCGCTGAGAGACACCAACTTCTGCGCGCGCGAGAACAGCGG 121
QY 44 ProProLeuLeuGlnIleGlyValSerLeuValValIleGluAspAspArgIle 63
Db 122 CGGCCCAAGCTGGGCAATCGTGGAGCAACGGGTTGTATTGAAGATGATGAGATT 181
QY 64 AsnAspValLeuValAsnMetThrAspValAlaPro-LeuValSerAsnSer-ProLeuTyr 83
Db 182 GATGACCTGCTGAAAATATGACAGACAGACGACCTCTCGGTCTTAATCTCCCAAGAA 241
QY 83 hrmMetSer 85
Db 242 CAATGACT 249

RESULT 15
CX122497 459 bp mRNA linear EST 21-DEC-2004
LOCUS NM02577 Mus Musculus lateral Ventricle Wall C57BL/6 adult Mus
DEFINITION musculus cDNA 5', mRNA sequence.
ACCESSION CX122497
VERSION CX122497.1 GI:56747285
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 459)
AUTHORS Williams, C., Wirta, W., Wikstrom, L., Lundberg, J. and Friesen, J.
TITLE Expressed sequence tags of cDNA clones from Mus Musculus Lateral
Ventricle Wall
JOURNAL Unpublished (2005)
COMMENT Contact: Williams, C.
Molecular Biotechnology
Institution of Biotechnology
Albanova University Center, KTH-Royal Institute of Technology, 106

91 Stockholm, Sweden
Tel: +4685537832.
Fax: +46855378481
Email: cecilia.williams@biotech.kth.se
Seq primer: M13FWD.
Location/Qualifiers
source 1..459
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/sex="Male and Female"
/tissue_type="Lateral Ventricle Wall"
/cell_type="Not applicable"
/dev_stage="Adult"
/lab_host="NeuroNova AB"
/clone_lib="Mus Musculus Lateral Ventricle Wall C57BL/6
adult"
/note="Organ: Brain; Vector: pCMVSPORT6; Site:1; Note:
Site 2: EORY, An oligo(dT) primed library was constructed
in pCMVSPORT6 from RNA isolated from lateral ventricle
wall tissue of adult male and female mice."

ORIGIN
Alignment Scores:
Pred. No.: 2.05e-43 Length: 459
Score: 396.00 Matches: 78
Percent Similarity: 95.2% Conservative: 1
Best Local Similarity: 94.0% Mismatches: 3
Query Match: 87.4% Indels: 1
DB: 8 Gaps: 0
US-10-071-645-2 (1-85) x CX122497 (1-459)

QY 1 MetTPGluValIleuProTyrGlyValAspGluValSerProTyrGlyValAsp 20
Db 74 ATGTGCGAGGTGCTGCCCTTACGCGACAGAGAGTGGCCCTTACGCGAGCGGCGGAC 133
QY 21 ValGlyGlnIlePheSerCysArgLeuGlnAspThrAsnAsnPhePheGlyValGlyGln 40
Db 134 GTGGCCAGATCTTCTGTGCGCGCTGCGAGACACCAACTTCTTGGGGCTGGGGCAG 193
QY 41 AsnValArgProProLeuLeuGlnIleGlyValSerLeuValValIleGluAsp 60
Db 194 AGCAAGCGGCTCCCAAGCTGGGCGAGATCGCGCGAGAGAGCGGCTGTATTGAAGAT 253
QY 61 AspArgGluLeuAspValLeuValAsnMetThrAspValAla-ProLeuValSerAsn 80
Db 254 GATGAGTTGATGACGTCGTAACACATGACAGACAGGACCCCTGTGTCTACTG 313
QY 80 rProlys 82
Db 314 CCCCAA 320

Search completed: March 9, 2006, 00:36:36
Job time: 3033 secs

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GenCore version 5.1.7
Copyright (C) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: March 8, 2006, 23:00:25 ; Search time 463 Seconds

(without alignments)
1223.540 Million cell updates/sec

Title: US-10-071-645-2

Sequence: 1 MMEVLYGDEKSPYGDGD.....VKNMTDKAPVNSPKTWS 85

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 496997 segs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-Q=/abs/ABSSWEB spool/US10071645/runat_08032006_115119_4599/abp_query.fasta_1
-DB=N Geneseq -QFT=fastcap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNTS=bits -START=1 -END=1 -MATRIX=blowum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=25 -MODE=LOCAL
-OUTFMT=plc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs804
-USER=US10071645 -CGEN 1.1 727 -@runat_08032006_115119_4599 -NCPU=6 -ICPU=3
-NO MAP -NRG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: N Geneseq 21:*

- 1: geneseqn1980a:*
- 2: geneseqn1990a:*
- 3: geneseqn2000a:*
- 4: geneseqn2001a:*
- 5: geneseqn2002a:*
- 6: geneseqn2003a:*
- 7: geneseqn2004a:*
- 8: geneseqn2005a:*
- 9: geneseqn2006a:*
- 10: geneseqn2007a:*
- 11: geneseqn2008a:*
- 12: geneseqn2009a:*
- 13: geneseqn2010a:*
- 14: geneseqn2011a:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	453	100.0	1104	6	AAD31052 Human PAP
2	413	91.2	553	8	ABX97604 cDNA enco
3	413	91.2	1581	4	AAC87358 Human dev
4	413	91.2	1620	14	AAE19389 Novel hum

5	413	91.2	1876	12	AD161702
6	413	91.2	1876	14	AAE43867
7	351	86.3	1533	13	ADU01554
8	290	64.0	3189	6	AAD31053
9	281	62.0	1510	2	AAE20426
10	281	62.0	1510	10	ADD90210
11	281	62.0	1510	10	ADD90029
12	281	62.0	1510	14	ADY25369
13	259.5	57.3	1222	10	ADD29744
14	253.5	56.0	450	14	AAE19537
15	253.5	56.0	550	6	ABK1646
16	241	53.2	183	3	AAE06461
17	229	50.6	549	12	ABT40422
18	229	50.6	549	12	ADP71513
19	199	43.9	869	6	ABO43206
20	199	43.9	869	6	ABO43207
21	197	43.5	869	6	ABO43208
22	197	43.5	869	6	ABO43209
23	186	43.3	255	8	ACC59221
24	186	43.3	2058	12	ADO24238
25	175	38.6	1850	11	ACN90200
26	172	38.0	1321	12	ADJ78198
27	172	38.0	1321	13	ADP25835
28	172	38.0	1321	13	ACC59222
29	149	32.9	129	8	ADU24606
30	128	28.3	229	10	ADU24606
31	128	28.3	474	9	ACB39424
32	111	24.5	434	13	ACR82616
33	94	20.8	65	6	ABN31583
34	83	18.3	65	6	ABN31772
35	74.5	16.4	8184	13	ADH84344
36	72	15.9	7122	13	ADH84502
37	72	15.9	7122	13	ADH84502
38	71.5	15.8	7122	13	ADH84466
39	71.5	15.8	447	4	AAH53864
40	71.5	15.8	654	6	ABN92893
41	71.5	15.8	654	13	ADSO1132
42	71.5	15.8	4218	4	AAH54841
43	71	15.7	10000	10	ADP77343
44	71	15.7	113306	10	ADH86554
45	70.5	15.6	1169	4	AAI27697

ALIGNMENTS

RESULT 1	
ID	AAD31052 standard; cDNA; 1104 BP.
XX	
XX	
AC	AAD31052;
XX	
DT	18-JUN-2002 (first entry)
XX	
DE	Human PAPAP cDNA.
XX	
KW	Human; PAPAP protein; schizophrenia candidate gene; g34872 gene;
KW	schizophrenia; bipolar disorder; central nervous system disorder;
KW	psychotic disorder; mood disorder; autism; mental retardation;
KW	psychiatric disease; anxiety disorder; impulse-control disorder;
KW	eating disorder; cognitive disorder; personality disorder; vaccine;
KW	chromosome 1p35-p36; neuroleptic; antipsychotic; tranquilizer;
KW	antidepressant; nootropic; antidiabetic; ss.
OS	Homo sapiens.
XX	
XX	
XX	
Key	Location/Qualifiers
FT	1..86
FT	/*tag= a
FT	87..344
FT	/*tag= b
FT	/product= "human PAPAP protein"
FT	345..1104
FT	/*tag= c

	TT	polyA_site	1085.._1104
	FT	/tag= d	
XX	PV		
XX	PN		
XX	PD		
XX	PP		
XX	PR		
XX	PA	(GSTR) GENSET.	
XX	PI	Bihain B , Bour B , Bougueleret L ;	
XX	DR	WFI : 2002-241732 /29 .	
XX	PT	P-PADB; AAE19431.	
XX	PT		
XX	XX	Novel isolated and purified or recombinant polynucleotide encoding PAPAP protein, useful for diagnosing and treating schizophrenia, bipolar disorder and other central nervous system disorders.	
XX	PS	Claim 2; Page 92; 96pp; English.	
XX	CC	The invention relates to human PAPAP polypeptides and polynucleotides.	
XX	CC	The invention also concerns the interaction of PAPAP with schizophrenia candidate gene g34872. PAPAP polypeptides, gene and anti-PAPAP antibodies are useful for treating schizophrenia, bipolar disorder or related central nervous system (CNS) disorders e.g. psychotic disorders, mood disorders, autism, substance dependence and alcoholism, mental retardation and other psychiatric diseases including cognitive, anxiety, eating, impulse-control and personality disorders. They are also used in vaccines. The present sequence is human PAPAP cDNA. The PAPAP gene is located on chromosome 1p35-p36	
XX	QO	Sequence 1104 BP; 350 A; 220 C; 262 G; 272 T; 0 U; 0 Other;	

Alignment Scores:	
Pred. No.:	1,12e-53
Score:	453.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	100.0%
DB:	6
Length:	1104
Matches:	85
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-071-645-2 (1-85) X AAD31052 (1-1104)

Qy	1	MecTrrpG1vValLeuPProTyrG1yAapG1uIyAylSeuSeProTyrG1yAapG1yG1yAap	20
Db	87	ATGCGAGAGGTCCTCCCTTAAGCGCGACGAGAAAGCTGAGAGCCCTTAAGCGAGAGCGCGCGAC	146
Qy	21	ValG1yG1nI1ePheSerCyAAGLeuG1nAapThrAapAapPhePheG1yAaG1yG1n	40
Db	147	GTCGGCCAGATCTTCTCCTGCGCCCTCGACGACACCAACATCTTTCGCGCGCGGCGAG	206
Qy	41	AenIyAaYpRProProLyLeuG1yG1nI1eG1yAerSerLyAaYpValI1eG1yAap	60
Db	207	AACCAAGCGCGCCCAACATCGCGCAGATCGCGCGACGAGCGGAGTGTGATTAAGAAGT	266
Qy	61	AspAaG11eAspAaPValLeuLyAaenMeThrAaPlyAaI1aProLeuValASerAenSer	80
Db	267	GATGAGATGAAGACGCTCGAAAAATATGACCCAGCAAGGACCTTCGTGTCTAACTCC	326
Qy	81	ProLyAaThrMeSer	85
Db	327	CCAAAGCAAAATAGT	341

```

RESULT 2
ABX97604
ID ABX97604 standard; cDNA, 553 BP
XX
AC ABX97604;
XX

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DT	16-MAY-2003	(first entry)	
DE	CDNA encoding novel human protein NOV9a.		
XX	Human; NOV; adrenoleukodystrophy; congenital adrenal hyperplasia; haemophilia; hypercoagulation; autoimmune disease; allergy; immunodeficiency; transplantation; Von Hippel-Lindau syndrome; Alzheimer's disease; stroke; tuberos sclerosis; hyperkalaemia; Parkinson's disease; Huntington's disease; cancer; fertility; diabetes; adult respiratory distress syndrome; infection; tissue typing; forensic identification; gene; 88.		
OS	Homo sapiens.		
FN	WO200290500-A2.		
PD	14-NOV-2002.		
XX	02-MAY-2002; 2002WO-US014256.		
PF	03-MAY-2001; 2001US-0288395P.		
XX	07-MAY-2001; 2001US-0289087P.		
PR	08-MAY-2001; 2001US-0289619P.		
PR	09-MAY-2001; 2001US-0289817P.		
PR	09-MAY-2001; 2001US-0289818P.		
PR	11-MAY-2001; 2001US-0290753P.		
PR	11-MAY-2001; 2001US-0290753P.		
PR	15-MAY-2001; 2001US-0291189P.		
PR	21-MAY-2001; 2001US-0292317P.		
PR	23-MAY-2001; 2001US-0293107P.		
PR	25-MAY-2001; 2001US-0293747P.		
PR	29-MAY-2001; 2001US-0294110P.		
PR	30-MAY-2001; 2001US-0294434P.		
PR	10-SEP-2001; 2001US-0318366P.		
PR	17-SEP-2001; 2001US-0322646P.		
PR	01-MAY-2002; 2002US-00136728.		
XX	(CUBA-) CUBAGEN CORP.		
PA	Spyrek KA, Li L, Edinger SR, Stone DJ, Guo X, Anderson DM; Pekturajan M, Gerlach VL, Raupler RJ, Pena CB, Padigaru M; Kellada R, Gorman L, Zernusen BD, Smithson G, MacDougall JR; Mezes PS, Feyman JA, Zhong M; WFI; 2003-103511/09.		
DR	P-PSDB; AB065229.		
XX	New NOV9a polypeptides and polynucleotides useful for treating or preventing e.g. congenital adrenal hyperplasia, hemophilia, hypercoagulation, autoimmune disease, allergies, immunodeficiencies, transplantation.		
PT	claim 1; Page 106-107; 300pp; English.		
XX	The invention describes an isolated polypeptide, NOV9a, comprising a sequence or a mature form of one of 21 51-1543 residue amino acid sequences (P1-221), given in the specification. The NOV9a polypeptides, polynucleotides and antibodies are useful in the manufacture of a medicament for treating or preventing e.g. adrenoleukodystrophy, congenital adrenal hyperplasia, haemophilia, hypercoagulation, autoimmune disease, allergies, immunodeficiencies, transplantation, Von Hippel-Lindau syndrome, Alzheimer's disease, stroke, tuberos sclerosis, hyperkalaemia, Parkinson's disease, Huntington's disease, cancer, fertility, diabetes, adult respiratory distress syndrome, viral, bacterial and parasitic infections. The nucleic acid sequences may be used in chromosome mapping, identifying individual from minute biological samples (tissue typing), and in forensic identification of a biological sample. This sequence encodes a novel human protein (NOV9a).		
XX	Sequence 553 BP; 169 A; 133 C; 170 G; 81 T; 0 U; 0 Other;		
XX	Alignment Scores: 1.97e-48 Length: 553		
XX	Accession No.: 1.97e-48 Length: 553		

Alignment Scores:	
Pred. No.:	1.97e-48
Length:	553

Score:	413.00	Matches:	84
Percent Similarity:	96.6%	Conservative:	0
Best Local Similarity:	96.6%	Mismatches:	1
Query Match:	91.2%	Indels:	2
DB:	8	Gaps:	0
US-10-071-645-2 (1-85) x ABX97604 (1-553)			
Qy	1 MetcrglnValIleuProTyrGlyAspGluYuleuSerProTyrGlnValIleuAsp	20	
Db	72 ATGCGAGAGTGTCTGCTTACGCGACAGAACTGAGCCCTTACGCGAGCGGCGAC	131	
Qy	21 ValGlnIleuPheSerCysAlaGluGlnAspThrAsnAspPheMetGlyAlaGln	40	
Db	132 GGGAGCCAGATCTCTCTGCTGCGCTGCAGACACACAACTTCTTGCGCGCGGCG	191	
Qy	41 AsnIleAspGlyProProlYaleuGlnIleGlyTyrGserIleAspValIleGluAsp	60	
Db	192 AACAAAGGCGCCGCCACAGCTGGCGAGTCGCGCGAGCAGACAGCGGCTGTATTAAG	251	
Qy	61 AspArgIleAspAspValIleuYsaanneThrAspIleValAProIleuValSerAsn	80	
Db	252 GATGAGTGTGAAGACGTGCTGAAATAATATGACCGACAGACGACCTCTCGTGTACTC	311	
Qy	80 r-ProlySerThrMetSer 85		
Db	312 CCCCAAGACATGAGT 328		
RESULT 3			
ID	AAC87358 standard; cDNA, 1581 BP.		
XX	AAC87358;		
XX	09-MAR-2001 (first entry)		
DE	Human developmentally-regulated hippocampus EST, SEQ ID NO:1.		
XX	Human hippocampal gene; hippocampus EST; expressed sequence tag;		
KW	developmental regulation; drug screening; modulator;		
KW	expression alteration; Alzheimer's disease; Huntington's disease;		
KW	Schizophrenia; epilepsy; diagnostic probe; gene therapy; neurotropic;		
XX	neuroprotective; anticonvulsant; neuroleptic; ss.		
OS	Homo sapiens.		
XX	WO200070036-A2.		
PD	23-NOV-2000.		
XX	10-MAY-2000; 2000WO-US013046.		
PF	17-MAY-1999; 99US-00313300.		
XX	(INCY-) INCYTE GENOMICS INC.		
XX	Kaser MR, Lal P, Yue H, Tang YT, Baughn MR, Azimzal Y;		
DR	WPI; 2001-016229/02.		
XX			
PT	Nucleic acids expressed in hippocampus useful for diagnosing, treating or		
PT	preventing diseases associated with the hippocampus, e.g., Alzheimer's		
PT	disease, Huntington's disease, Schizophrenia and epilepsy.		
PS	Claim 2; Page 31; 39pp; English.		

CC	human developmentally-regulated hippocampal gene; recombinant production
CC	of the genome product; and a method of screening for a compound which
CC	specifically binds to a human hippocampal gene of the invention or its
CC	product. It additionally encompasses nucleic acid sequences with at least
CC	70% identity to one of the human hippocampal ESTs, and proteins with at
CC	least 85% identity to the human hippocampal protein of the invention. The
CC	human hippocampal genes, their encoded proteins and modulators of the
CC	genes or proteins are useful for treating or preventing diseases
CC	associated with altered expression of a gene in the hippocampus, such as
CC	Alzheimer's disease, Huntington's disease, schizophrenia, epilepsy and
CC	complications thereof of these conditions. The nucleic acid sequences, or
CC	fragments thereof are also as hybridisation probes for use in diagnosing
CC	a disease or condition associated with altered expression of a
CC	hippocampal gene. The present sequence represents a human hippocampal EST
CC	corresponding to a developmentally-regulated gene of the invention
XX	
SQ	Sequence 1581 BP; 500 A; 307 C; 325 G; 449 T; 0 U; 0 Other;
Alignment Scores:	
Pred. No.:	7,88e-48 Length: 1581
Score:	413.00 Matches: 84
Percent Similarity:	96.6% Conservative: 0
Best Local Similarity:	Mismatches: 1
Query Match:	Gaps: 2
DB:	Indels: 0
	Gaps: 0
US-10-071-645-2 (1-85) x MAC87358 (1-1581)	
QY	1 MetTgplValIleauPcFqrgtYApAGlYLeuSerProTyrgtYApdLYGtYASP 20
Dd	39 ATGTGGAGAGCTCTCGCCTTCACGCACACAAACTTAGCCCTTCAGCACGGCGGCAC 98
QY	21 ValIGVlnIIepheSeCYsArYLEuGIInAsPTThraMaenPhPeGtVALaGLYGlN 40
Dd	99 GTGGCGCAATCTTCTCTCTCGCCTTGAGAACACCAACAACCTTTCTGCGCGCGGAG 158
QY	41 AsnLYsAqPPROPpOLysLEuGIYGlInIEGLYAgsErlYsAgVAValIIeGLIsuAP 60
Dd	159 AACAAACGCCGCCCAAAGCTGGGCACAGTGGCGGACGAACGCGGTGTATTATMAAT 218
QY	61 AspArgILeaSPaPVallleuYsaMeTHrasPLYsALaPRO-leuValSErSaNsE 80
Dd	219 GAATGCAATGTATGACGTCGTGAAAATAATGACGACAAAGGACCTCTGTGTAACTC 278
QY	80 r-ProLYseTHMetSer 85
Dd	279 CCCCAAGCAATGAGT 295
RESULT 4	
ID	AEA19389 standard; cDNA; 1620 BP.
AC	AEA19389;
XX	
XT	11-AUG-2005 (first entry)
DE	Novel human polynucleotide SEQ ID NO 83.
KW	vulnerary; CNS-gen.; gene therapy; diagnostic; forensic; mapping;
KM	DNA purification; protein purification; osteoarthritis; arthritis;
KM	osteoporosis; musculoskeletal disease; osteoporosis; endocrine disease;
KM	periodontal disease; antiinflammatoxy; mouth disease; burns; injury;
KM	peripheral neuropathy; Alzheimer's disease; neuroprotective; noctropia;
KM	dementia; Parkinson's disease; antiparkinsonian; neurological disease;
KM	cerebrovascular ischemia; cerebroprotective; vasotropic;
KM	cardiovascular disease; autoimmune disease; immunosuppressive;
KM	immune disorder; viral infection; vinnicide; infection; cancer;
KM	cytostatic; neoplasm; gene; ss.
OS	Homo sapiens.
NN	WO2005049806-A2.
XX	

XX 02-JUN-2005.
XX
XX 11-MAR-2004; 2004MO-US007412.
XX
XX PR
XX 14-MAR-2003; 2003US-00389559.
XX
XX (NIVE-) NOVELO INC.
XX PA
XX Tang TY, Wang J, Wang ZW, Zhang J, Ren F, Zhou P, Ma Y;
XX PT Ghosh W, Xue A, Asundi V, Zhao Q, Wang D, Goodrich R, Chen R,
XX PT Weinman T, Weng G, Boyle B;
XX DR MPI; 2005-417730/42.
XX P-PSDB; AEA19956.
XX
XX New polynucleotide encoding a polypeptide with biological activity,
XX useful for treating a disease or disorder, e.g. osteoarthritis, burns,
XX CNS and peripheral disease, stroke, autoimmune disorders, viral
XX infection, or cancer.

Claim 1; SEQ ID NO 83; 500bp; English.

The invention describes a new isolated polynucleotide (1) encoding a polypeptide with biological activity comprising: a nucleotide sequence of SEQ ID NOS: 1-567 (fully defined); a nucleotide sequence that hybridizes to the sequence of (1) under stringent hybridization conditions; or a nucleotide sequence having greater than 9% sequence identity with the sequence of (1). Also described are: a(n) (expression) vector comprising (1); a host cell genetically engineered to comprise (1) operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell; an isolated polypeptide comprising a sequence of SEQ ID NOS: 568-1134 (fully defined), where the polypeptide is: a polypeptide encoded by (1); or a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NOS: 1-567; a composition comprising the polypeptide of (3) and a carrier; an antibody directed against the polypeptide of (3); a method for detecting (1) in a sample; a method for producing the polypeptide of (3) in a sample; a method for identifying a compound that binds to the polypeptide of (3); a method for producing the polypeptide of (3); and a collection of polynucleotides, where the collection comprising of at least one of SEQ ID NOS: 1-567. (1) is a polynucleotide comprising any of the sequences of SEQ ID NOS: 1-567 encoding a polypeptide with biological activity, which comprises any of the amino acid sequence of SEQ ID NOS: 568-1134. All sequences are fully defined in the specification. The sequences and methods are useful in diagnostics, forensic, and gene mapping, in identifying of mutations responsible for genetic disorders or other traits, in assessing biodiversity, and for producing many other types of data and products dependent on DNA and amino acid sequences. The composition and method are useful for treating a disease or disorder, e.g., osteoporosis, osteoarthritis, periodontal disease, burns, CNS and peripheral disease, Alzheimer's disease, Parkinson's disease, stroke, autoimmune disorders, viral infection, or cancer. This sequence encodes a novel polypeptide of the invention.

Sequence 1620 BP; 409 A; 415 C; 452 G; 344 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Length:	Matches:
Score:	8, 14e-48	1620
Percent Similarity:	413.00	84
Best Local Similarity:	96.6%	Conservative: 0
Query Match:	91.2%	Mismatches: 1
DB:	14	Indels: 2
		Gaps: 0

US-10-071-645-2 (1-85) x AEA19389 (1-1620)

QY 1 MetTPGIVAlIlePrOTyTGYAASPIyUlySeusePrOTyTGYAASPIyGIYAAP 20

DB 454 ATGTGGAGGGTGTCCTCGCCGACGAAGAAGTCAAGCCTCGACGCGCGGCAC 5133

QY 21 ValIGVgInIlePhesrCYeArGLauGIgharPhraAsnPhPheNGValagIvGIin 40

DB 514 GTGGGCCAAATCTCTCTCTGCGCGCTCGACGACCAACAACACTCTTGTGGCGCCGGCG 5738

Oy		4	AsnLTAAATGACGGCGCCCAAGCTGGGCCAAGTGGCGGAGCAGACGGGTATTATGAAGAT	633
Dd		574	AACACCGCGCGCCCAAGCTGGGCCAAGTGGCGGAGCAGACGGGTATTATGAAGAT	633
Oy		61	AspAphxIIIsaaApayVLIleuYsaAmcThrAspLyAlaPro-IleuValSerPase	80
Dd		634	GATGGATTGATGAGTGCTGTAATAATATGACGACAGGCACCCTCGATGTCCTACTC	693
Oy		80	T-ProlystHrmctSer	85
Dd		694	CCCCAAGACCATGATGAT	710
RESULT 5				
ID	AD161702	standard; cDNA; 1876 BP.		
AC	AD161702;			
DT	22-APR-2004	(first entry)		
XX		Human cDNA downregulated in Alzheimer's disease, INCYTE 234151.1.		
KW	Human; ss; Alzheimer's disease; differential display; neuroprotective;			
KX	brain disorder.			
OS	Homo sapiens.			
PX	US6682886-B1.			
PD	27-JAN-2004.			
KX	05-MAY-2000; 2000UTS-00566921.			
PF				
PR	05-MAY-2000; 2000UTS-00566921.			
PA	(INCY-) INCYTE CORP.			
XK	Loring JF, Tingley DW, Edwards CM;			
P1	WPI; 2004-118572/12.			
PT	New composition comprising cDNAs that are differentially expressed in			
PS	brain disorders, useful for diagnosing or treating Alzheimer's disease.			
PS	Claim 1; SEQ ID NO 70; 223bp; English.			
XX				
CC	The invention relates to a new composition comprising AD161633-			
CC	AD161770and their complements that are cDNAs differentially expressed in			
CC	brain disorders. Also included are a high throughput method for detecting			
CC	differential expression of one or more cDNAs in a sample containing			
CC	nucleic acids and a high throughput method for screening a library of			
CC	molecules or compounds to identify a ligand that specifically binds a			
CC	cDNA. The expression of the each of the cDNAs is downregulated at least			
CC	two-fold in the brain of the subjects with Alzheimer's disease (AD161633-			
CC	AD161727) or upregulated at least two fold in Alzheimer's disease			
CC	(AD161728-AD161770). The composition is useful for diagnosing or treating			
CC	Alzheimer's disease. The present sequence is a cDNA downregulated at			
CC	least two-fold in the brain of the subjects with Alzheimer's disease.			
SQ	Sequence 1876 BP; 480 A; 442 C; 442 G; 480 T; 0 U; 32 Other;			
Alignment Scores:				
Pred. No. :	9,88e+48	Length:	1876	
Score:	413.00	Matches:	84	
Percent Similarity:	96.64	Conservative:	0	
Best Local Similarity:	96.64	Mismatches:	1	
Query Match:	91.24	Indels:	2	
DB:	12	Gaps:	0	
OY	US-10-071-645-2 (1-85) x AD161702 (1-1876)			
OY	1 MetrcplvalalleuPrOtyrGylapogulysleusserPrOtyrGilyaspGilyalysp			20

DB 355 ATGTGGAGGTGCTGCTTACGCGCAGACCAAGCTTACGCTTACGCGCAGC 414
QY 21 ValGlyGlnIlePheSerCysArgLeuGlnAspThrAsnaMphPheGlyAlaGlyGln 40
DB 415 GTGGGCCAGATCTTCTCCGCGCTCAGGACCAACACTTCTTCCGCGCGGCGCAG 474
QY 41 AsnLysArgProProlYsLeuGlnIleGlyArgSerLysArgValAlaIleGluAsp 60
DB 475 AACACAGCGCGCCGCCAACGCTGGCGCAGATCGCCGCGGACGCGGTTGTTATGGAAGT 534
QY 61 AsparGlleAspAspValIleuLysAsnMetThrAspLysAlaPro-LeuValSerAsnSe 80
DB 535 GATGAGATTGATGACCTGCTGAAAATATGACCGACAGGACCTCTCGGTGCTTAATC 594
QY 80 r-ProlyerThMetSer 85
DB 595 CCCCAAGACATGAGT 611
RESULT 6
ID AEA43867
AC AEA43867 standard; cDNA; 1876 BP.
XX AEA43867;
XX
DT 25-AUG-2005 (first entry)
XX
DE Human CDNA differentially expressed in brain tissue SEQ ID NO:70.
XX
KW diagnosis; treatment; brain disease; neuroprotective; cerebroprotective;
KW muscular-gen.; cytostatic; neuroleptic; nootropic; antidepressant;
KW anticonvulsant; analgesic; antiparkinsonian; ophthalmological;
KW immunotherapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN US2005130171-A1.
XX
PD 16-JUN-2005.
XX
PF 26-JAN-2004; 2004US-00765700.
XX
PR 05-MAY-2000; 2000US-00566921.
XX
PA (INCY-) INCYTE CORP.
XX
PI Loring JF, Tingley DW, Edwards CM;
XX
DR MPI; 2005-456990/46.
XX
PT Composition useful for diagnosis, staging, treating or monitoring
PT treatment of a subject with a brain disorder; comprises several cDNAs
PT that are differentially expressed in brain disorders.
XX
PS Claim 1; SEQ ID NO 70; 231bp; English.
XX
CC The invention relates to a composition (I) for the diagnosis, staging,
CC treatment or for the monitoring of treatment of a subject with a brain
CC disorder. (I) comprises several cDNAs that are differentially expressed
CC in brain disorders and chosen from any one of 138 nucleotide sequences of
CC AEA43798-EA43935, or their complements. Also described: (1) a high
CC throughput method for detecting differential expression of one or more
CC cDNAs in a sample containing nucleic acids; (2) an isolated cDNA (II)
CC selected from AEA43812, AEA43813, AEA43830, AEA43831, AEA43855, AEA43856,
CC AEA43883 and AEA43923; (3) an expression vector (III) containing (II);
CC (4) a host cell (IV) containing (III); (5) a protein (V) produced using
CC (IV); and (6) a pharmaceutical composition comprising (V). (I) is useful
CC for a high throughput method of screening a library of molecules or
CC compounds to identify a ligand which specifically binds a cDNA, where the
CC method involves combining (I) with the library of molecules or compound
CC under conditions to allow specific binding and detecting specific binding
CC between each cDNA and a molecule or compound. (IV) is useful for
CC producing a protein, which involves culturing (IV) under conditions for

CC the expression of the protein and recovering the protein from the
CC culture. (V) is useful for high throughput method for screening a library
CC of molecules or compounds to identify a ligand which specifically binds
CC (V), where the method involves combining (V) or its portion with the
CC library of molecules or compound under conditions to allow specific
CC binding and detecting specific binding between (V) and a molecule or
CC compound. (V) is useful for purifying a ligand from a sample, which
CC involves combining (V) or its portion with the sample under conditions to
CC allow specific binding, recovering the bound protein and separating the
CC protein from ligand. (V) is also useful for producing an antibody, which
CC involves immunizing an animal with (V) or its portion under conditions to
CC elicit an antibody response, isolating animal antibodies and screening
CC for the treatment or prevention of conditions and disorders associated
CC with immune response. The present sequence represents a human cDNA
CC sequence which is differentially expressed in brain tissues, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 1876 BP; 480 A; 442 C; 442 G; 480 T; 0 U; 32 Other.
XX
Alignment Scores:
Pred. No.: 9,886-48 Length: 1876
Score: 413.00 Matches: 84
Percent Similarity: 96.6% Conservative: 0
Best Local Similarity: 96.6% Mismatches: 1
Query Match: 91.2% Indels: 2
DB: 14 Gaps: 0
US-10-071-645-2 (1-85) x AEA43867 (1-1876)
QY 1 MetTrpGluValIleuProTyrGlyAspGluLysSerProTyrGlyAspGlyGlyAsp 20
DB 355 ATGTGGAGGTGCTGCTTACGCGCAGACCAAGCTTACGCTTACGCGCAGC 414
QY 21 ValGlyGlnIlePheSerCysArgLeuGlnAspThrAsnaMphPheGlyAlaGlyGln 40
DB 415 GTGGGCCAGATCTTCTCCGCGCTCAGGACCAACACTTCTTCCGCGCGGCGCAG 474
QY 41 AsnLysArgProProlYsLeuGlnIleGlyArgSerLysArgValAlaIleGluAsp 60
DB 475 AACACAGCGCGCCGCCAACGCTGGCGCAGATCGCCGCGGACGCGGTTGTTATGGAAGT 534
QY 61 AsparGlleAspAspValIleuLysAsnMetThrAspLysAlaPro-LeuValSerAsnSe 80
DB 535 GATGAGATTGATGACCTGCTGAAAATATGACCGACAGGACCTCTCGGTGCTTAATC 594
QY 80 r-ProlyerThMetSer 85
DB 595 CCCCAAGACATGAGT 611
RESULT 7
ID ADD001554
AC ADD001554 standard; cDNA; 1533 BP.
XX ADD001554;
XX
DT 27-JAN-2005 (first entry)
XX
DE Novel human polynucleotide seqid 21.
XX
KW cytostatic; antiproliferative; antiinflammatory; gene therapy; Nanodisc;
KW proliferative disorder; inflammatory disorder; immune disorder;
KW metabolic disorder; bone disorder; CNS disorder; cancer; psoriasis;
KW ulcerative colitis; human; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004093804-A2.
XX
PF 04-NOV-2004.
XX
PR 19-APR-2004; 2004WO-US012047.
XX

18-APR-2003; 2003US-0463708P.
PR 18-APR-2003; 2003US-0463732P.
PR 02-MAY-2003; 2003US-0467135P.
PR 02-MAY-2003; 2003US-0467232P.
PR 19-MAY-2003; 2003US-0471306P.
PR 19-MAY-2003; 2003US-0471336P.
PR 08-JUL-2003; 2003US-0483223P.
PR 08-JUL-2003; 2003US-0483224P.
PR 14-JUL-2003; 2003US-0486446P.
PR 14-JUL-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.
PR 08-SEP-2003; 2003US-0505059P.
XX
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.
XX
XX Lee E, Heetir K, Chu K, Masuoka L, Williams LT;
XX MPI; 2004-775861/76.
XX P-PSDB; ADU02286.
XX
XX New first nucleic acid molecule comprising a polynucleotide sequence
PT given in the specification, useful in preparing a composition for
PT diagnosing or treating e.g., cancer, psoriasis or ulcerative colitis.
XX
XX Claim 1; SEQ ID NO 21; 291pp; English.
XX
XX The invention describes a new first nucleic acid molecule comprising a
CC polynucleotide sequence given in the specification. Also described are:
CC an animal injected with the nucleic acid molecule; a second nucleic acid
CC molecule comprising a second polynucleotide sequence that is at least
CC about 70, 80, 90 or 95% homologous to the first nucleic acid molecule or
CC that hybridises to the first polynucleotide sequence under high
CC stringency conditions; a vector comprising the nucleic acid molecule; a
CC promoter that drives the expression of the nucleic acid molecule; a
CC host cell transformed, transfected, transduced or infected with the
CC nucleic acid molecule; a nucleic acid composition comprising a carrier or
CC a buffer and one or more compositions comprising the nucleic acid
CC molecule, vector or host cell; a substantially purified polypeptide; an
CC animal injected with the polypeptide; a carrier or buffer; a cell
CC comprising the polypeptide molecule and a carrier or buffer; a cell
CC culture medium comprising the polypeptide or transfected cells
CC transfected with the polynucleotide; making a transformed, transfected,
CC transduced, or infected host cell; synthesising Nanodiscs simultaneously
CC and for synthesising a series of simultaneously-synthesised Nanodiscs
CC sequentially utilising a dynamic system; preparing a hydrophobic protein
CC for determination of crystal structure; immunising a non-human animal;
CC screening for modulators of hydrophobic protein activity; a diagnostic
CC kit; determining the presence of the nucleic acid molecule or its
CC complement; determining the presence of an antibody to the polypeptide in
CC a sample; an antibody specifically recognising, binding to or modulating
CC the biological activity of at least one polypeptide encoded by a nucleic
CC acid molecule or its biologically active fragment; an antibody
CC composition comprising the antibody and a carrier; a bacteriophage, where
CC the antibody is displayed on the bacteriophage; a non-human animal injected with the
CC antibody composition; a host cell that secretes the antibody; making an
CC antibody; diagnosing a disease, disorder, syndrome, or condition
CC comprising cancer, or proliferative, inflammatory, immune, metabolic,
CC bone, CNS, genetic, bacterial and viral diseases, disorders, syndromes or
CC conditions in a patient; a modulator composition comprising a modulator
CC and a carrier; gene therapy; prophylactic or therapeutic treatment of a
CC subject; an isolated modified cell comprising at least one first
CC heterologous nucleic acid molecule, where the first heterologous nucleic
CC acid molecule comprises a first polynucleotide sequence that encodes a
CC first polypeptide; a non-human animal deficient in the polypeptide or
CC that over-expresses the polypeptide, isolated tissues derived from the
CC non-human animal; and one or more cells derived from the non-human
CC animal. The nucleic acid is useful in preparing a composition for
CC diagnosing or treating e.g., cancer, psoriasis or ulcerative colitis.
XX This sequence encodes a novel human polypeptide of the invention.
XX
XX Sequence 1533 BP; 329 A; 444 C; 479 G; 261 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9,6e-45 Length: 1533
Score: 391.00 Matches: 74
Percent Similarity: 98.7% Conservative: 0
Best Local Similarity: 98.7% Mismatches: 1
Query Match: 86.3% Indels: 0
DB: 13 Gaps: 0
US-10-071-645-2 (1-85) x ADU01554 (1-1533)
QY 1 MetTpgGluValIleuProTyrGlyAspGluLeuSerProTyrGlyAspGlyValAsp 20
DB 1300 ATGTGGAGGTGCTGCTGCTCAAGCGAGAGAGAGCTAGGCTTACGGCGAGCGGCGAG 1359
QY 21 ValGlyGlnIlePheSerCysArgLeuGlnAspThrAsnAsnPhaGlyAlaGlyGln 40
DB 1360 GTGGCCAGATCTTCTTCTGCGCTGCGAGACCAACACTTCTTGGCGCGGCGAG 1419
QY 41 AsnIlyAspGProProIleLeuGlyGlnIleGlyArgSerIlyArgValIleGluAsp 60
DB 1420 AACAAAGCGGCGCGCCAGAGCGGCGAGATCGCGCGAGACGCGGCTTATTGAAGAT 1479
QY 61 AspArgIleAspAspValIleuIlyAsnMetThrAspIlyAlaPro 75
DB 1480 GATAGGATTGATGACGTGCTGAAATATGACGACAGCAAGCACT 1524
RESULT 8
AD31053
ID AD31053 standard; DNA, 3189 BP.
XX
XX AD31053;
AC
AC 18-JUN-2002 (first entry)
DT
DT
XX
XX Human PAPAP gene.
DE
XX
XX Human; PAPAP protein; schizophrenia candidate gene; g34872 gene;
KW schizophrenia; bipolar disorder; central nervous system disorder;
KW psychotic disorder; mood disorder; autism; mental retardation;
KW psychiatric disease; anxiety disorder; impulse-control disorder;
KW eating disorder; cognitive disorder; personality disorder; vaccine;
KW chromosome 1p35-p36; neuroleptic; antiaconollic; tranquilliser;
KW antidepressant; nootropic; antiaddictive; ds.
XX
XX Homo sapiens.
OS
OS
XX WO200212279-A2.
PN
PN 14-FEB-2002.
PD
PD 26-JUN-2001; 2001WO-IB001891.
PF
PF 07-AUG-2000; 2000US-0223482P.
PR
PR
XX (GEST) GENSET.
PA
PA
XX Bihain B, Bour B, Bougueleret L;
PI
PI MPI; 2002-241732/29.
DR
DR
XX Novel isolated and purified or recombinant polynucleotide encoding PAPAP
PT protein, useful for diagnosing and treating schizophrenia, bipolar
PT disorder and other central nervous system disorders.
XX
XX Disclosure; Page 93-94; 96pp; English.
PS
PS The invention relates to human PAPAP polypeptides and polynucleotides.
XX The invention also concerns the interaction of PAPAP with schizophrenia
CC candidate gene g34872. PAPAP polypeptides, gene and anti-PAPAP antibodies
CC are useful for treating schizophrenia, bipolar disorder or related
CC central nervous system (CNS) disorders e.g. psychotic disorders, mood
CC disorders, autism, substance dependence and alcoholism, mental


```
OS Homo sapiens.
XX US2003196683-A1.
XX
XX 23-OCT-2003.
XX
XX 30-MAR-2001; 2001US-00820649.
XX
XX 30-JUL-1997; 97US-0054209P.
XX 30-JUL-1997; 97US-0054211P.
XX 30-JUL-1997; 97US-0054212P.
XX 30-JUL-1997; 97US-0054213P.
XX 30-JUL-1997; 97US-0054214P.
XX 30-JUL-1997; 97US-0054215P.
XX 30-JUL-1997; 97US-0054217P.
XX 30-JUL-1997; 97US-0054218P.
XX 30-JUL-1997; 97US-0054234P.
XX 30-JUL-1997; 97US-0054236P.
XX 18-AUG-1997; 97US-0055968P.
XX 18-AUG-1997; 97US-0055972P.
XX 18-AUG-1997; 97US-0056534P.
XX 19-AUG-1997; 97US-0056543P.
XX 19-AUG-1997; 97US-0056549P.
XX 19-AUG-1997; 97US-0056561P.
XX 19-AUG-1997; 97US-0056727P.
XX 19-AUG-1997; 97US-0056729P.
XX 19-AUG-1997; 97US-0056730P.
XX 29-JUL-1998; 98MO-US015949.
XX 26-JAN-1999; 99US-00236557.
XX 21-SEP-2000; 2000US-0066987.
XX
XX (RUBE/) RUBEN S M.
XX (FENG/) FENG P.
XX (LAFLE/) LAFLEUR D W.
XX (MOOR/) MOORE P A.
XX (SHIY/) SHI Y.
XX (KYAW/) KYAW H.
XX (LIYY/) LI Y.
XX (ZENG/) ZENG Z.
XX (CART/) CARTER K C.
XX (ENDR/) ENDRESS G A.
XX (WEIY/) WEI Y.
XX (FANP/) FAN P.
XX (ROSE/) ROSEN C A.
XX
XX Ruben SM, Feng P, Lafleur DW, Moore PA, Shi Y, Kyaw H, Li Y;
XX Zeng Z, Carter KC, Endress GA, Wei Y, Fan P, Rosen CA;
XX WPI: 2003-852813/79.
XX P-PSDB; ADP90301.
XX
XX New nucleic acid molecule, useful for preparing a medicament for
XX preventing, treating or ameliorating a medical condition e.g., cancer.
XX
XX Claim 1; SEQ ID NO 25; 213bp; English.
XX
XX The invention describes novel isolated human nucleic acids. The nucleic
XX acid is useful for preparing a medicament for preventing, treating or
XX ameliorating a medical condition e.g., cancer, and in gene therapy. This
XX sequence encodes a novel human secreted protein of the invention.
XX
XX Sequence 1510 BP; 473 A; 285 C; 299 G; 450 T; 0 U; 3 Other;
SQ
Alignment Scores:
Pred. No.: 3,1e-29 Length: 1510
Score: 281.00 Matches: 64
Percent Similarity: 92.8% Conservative: 0
Best Local Similarity: 92.8% Mismatches: 3
Query Match: 62.0% Indels: 3
DB: 10 Gaps: 0
US-10-071-645-2 (1-85) x ADP90210 (1-1510)
```

```
QY 19 G1YAspValG1Yg1n1lePheSerCyAArgLeuG1nAspThrAanAanPheG1YAla 38
Db 2 GGCGACGTCGGCCAGATCTCTCTCCGCGCCGCGCAGNCCACCAACACTCTCGAGCCG 61
QY 39 G1Yg1nAsn1YsArgProProLYsLeuG1Yg1n1leG1YArgSerLYsArgVal11le 58
Db 62 GGCGAGAAACAGCGCGCCGCAAG-CTGGCGAGATCGCCGAGCAAGCGGGTTGTTATT 120
QY 59 G1uAspAspArg11eAspAspVal1leuLYsAsnMetThrAspLYsAlaPro-LeuValSe 78
Db 121 GAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
QY 78 rAnSer-ProLYSThrMetSer 85
Db 181 TAACTCCGCCAAGACATGAGT 203
RESULT 11
ADG90029
ID ADG90029 strand; cDNA; 1510 BP.
XX
XX ADG90029;
XX
XX 11-MAR-2004 (first entry)
XX
XX Human cDNA from secreted protein gene 15.
XX
XX Secreted protein; gene therapy; neural disorder; immune system disorders;
XX muscular disorder; reproductive disorder; gastrointestinal disorder;
XX pulmonary disorder; cardiovascular disorder; renal disorder;
XX proliferative disorder; cancer; systemic lupus erythematosus;
XX rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
XX Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
XX Parkinson's disease; Alzheimer's disease; atherosclerosis;
XX myocardial infarction; AIDS; infection; human; ss; gene.
XX
XX Homo sapiens.
XX
XX US2003166541-A1.
XX
XX 04-SEP-2003.
XX
XX 04-JUN-2002; 2002US-00160162.
XX
XX 30-JUL-1997; 97US-0054209P.
XX 30-JUL-1997; 97US-0054211P.
XX 30-JUL-1997; 97US-0054212P.
XX 30-JUL-1997; 97US-0054213P.
XX 30-JUL-1997; 97US-0054214P.
XX 30-JUL-1997; 97US-0054215P.
XX 30-JUL-1997; 97US-0054217P.
XX 30-JUL-1997; 97US-0054218P.
XX 30-JUL-1997; 97US-0054234P.
XX 30-JUL-1997; 97US-0054236P.
XX 18-AUG-1997; 97US-0055968P.
XX 18-AUG-1997; 97US-0055972P.
XX 18-AUG-1997; 97US-0056534P.
XX 19-AUG-1997; 97US-0056543P.
XX 19-AUG-1997; 97US-0056549P.
XX 19-AUG-1997; 97US-0056561P.
XX 19-AUG-1997; 97US-0056727P.
XX 19-AUG-1997; 97US-0056729P.
XX 19-AUG-1997; 97US-0056730P.
XX 29-JUL-1998; 98MO-US015949.
XX 26-JAN-1999; 99US-00236557.
XX 05-JUN-2001; 2001US-0295558P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Feng P, Lafleur DW, Moore PA, Shi Y, Kyaw H, Li Y;
XX Zeng Z, Carter KC, Endress GA, Wei Y, Fan P, Rosen CA;
```

DR WPI: 2003-874923/81.
 DR P-PSDB; ADG90120.
 PT Nucleic acid encoding 83 secreted polypeptides, useful for preventing,
 PT diagnosing and treating disorders related to their aberrant expression
 PT and activity.
 XX
 PS Claim 1; SEQ ID NO 25; 308bp; English.
 CC
 CC The invention relates to an isolated nucleic acid molecule encoding a
 CC secreted protein that is at least 95% identical to a polynucleotide
 CC fragment of any of the nucleotide sequences listed in table 1A of the
 CC specification, which is hybridizable to the nucleotide sequences, a
 CC polynucleotide encoding a polypeptide (or a polypeptide fragment, a domain
 CC or epitope of any of the amino acid sequences) listed in table 1A of the
 CC specification, a polynucleotide which is an (allelic) variant of the
 CC nucleotide sequences listed in the above amino acid sequences, a
 CC polynucleotide capable of hybridizing under stringent conditions to any
 CC of the above polynucleotides, where the polynucleotide does not hybridize
 CC under stringent conditions to a nucleic acid molecule having a nucleotide
 CC sequence of only A or T residues. Also included are a recombinant vector
 CC comprising the above nucleic acid molecule, an isolated polypeptide
 CC cell comprising the above nucleic acid molecule, an isolated polypeptide
 CC (or its fragment, domain, epitope, secreted form, (allelic) variant or
 CC homologue) encoded by the above nucleic acid molecule, an isolated
 CC antibody that binds specifically to the above polypeptide, a recombinant
 CC host cell produced by the above method and that expresses the above
 CC polypeptide, making an isolated polypeptide, preventing, treating or
 CC ameliorating a medical condition, diagnosing a pathological condition or
 CC a susceptibility to a pathological condition in a subject, identifying a
 CC binding partner to the above polypeptide, the gene corresponding to the
 CC cDNA sequence given in the specification, and identifying an activity in
 CC a biological assay. The nucleic acid molecule and polypeptide are useful
 CC in diagnosing, preventing, prognosis and/or activity of the above
 CC associated with aberrant expression and/or activity of the above
 CC polypeptide, such as neural disorders, immune system disorders, muscular
 CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
 CC disorders, cardiovascular disorders, renal disorders, proliferative
 CC disorders and/or cancers. In particular, these diseases are systemic
 CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis,
 CC thyroiditis, anemia, Grave's disease, diabetes, hepatitis, asthma,
 CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
 CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
 CC may be used for identifying agonists and antagonists of the
 CC polynucleotide and polypeptide. The present sequence is a cDNA from one
 CC of the 83 disclosed secreted protein genes.
 XX
 SQ Sequence 1510 BP; 473 A; 285 C; 299 G; 450 T; 0 U; 3 Other;
 Alignment Scores:
 Prod. No.: 3 1e-29 Length: 1510
 Score: 281.00 Matches: 64
 Percent Similarity: 92.8% Conservative: 0
 Best Local Similarity: 92.8% Mismatches: 3
 Query Match: 62.0% Indels: 3
 DB: 10 Gaps: 0
 US-10-071-645-2 (1-85) x ADG90029 (1-1510)
 QY 19 G1yapva1g1yln1lpheserCyakrglenglnasPthAasnaaphegiyala 38
 DB 2 G3GACGCTG3G3CAGATCTTCTCCGCGCTCAGACACCAACATCTTCCGCGCC 61
 QY 39 G1ylnasnlYsArpProFrolylsleuG1yln1lglYArSerLYaRgVAlval1le 58
 DB 62 GGGCAGAAACAAGCGCGCCCAAG-CTGGCGCAAGATCGCGCGAGCAGCGGGTGTATT 120
 QY 59 G1uapapapAr1g1leapapavAlleu1yAsnmeCThraspLYa1a1pro-LeuValse 78
 DB 121 GAAAGATATAGATGATGACGCTGCTGAAATAATATGACGACAGACACCTCCGTGTC 180

QY 78 rAnSer-ProlyThrMetSer 85
 DB 181 TACTCTCCCAAGACATAGT 203
 RESULT 12
 ADY25369
 ID ADY25369 standard; cDNA; 1510 BP.
 AC ADY25369;
 XX
 DT 05-MAY-2005 (first entry)
 XX
 DE Novel human secreted protein-encoding cDNA SeqID25.
 XX
 KW Cancer; cytostatic; arthritis; antiarthritic; asthma; antiasthmatic;
 KW acquired immune deficiency syndrome; rheumatoid arthritis; anti-rheumatic;
 KW inflammatory bowel disease; anti-inflammatory; gastrointestinal-gen.;
 KW sepsis; antibacterial; immunosuppressive; acne; anti-seborrheic;
 KW dermatological; psoriasis; antipsoriatic; atherosclerosis;
 KW antiarteriosclerotic; cerebrovascular ischemia; cerebroprotective;
 KW vasotropic; thrombotic; wound healing; vulnery; Alzheimer's disease;
 KW neuroprotective; noctropic; parkinson's disease; antiparkinsonian; autism;
 KW obsessive-compulsive disorder; tranquilizer; graft versus host disease;
 KW immune disorder; hematological disease; inflammation; infection;
 KW hyperproliferative disorders; renal disease; nephrotropic;
 KW cardiovascular disease; cardiovascular-gen.; respiratory disorder;
 KW neurological disease; neuroprotective; endocrine disease;
 KW reproductive disorders (General); gynecological; gene; ss.
 XX
 XX Homo sapiens.
 XX
 XX US2005037467-A1.
 XX 17-FEB-2005.
 XX
 PF 09-SEP-2004; 2004US-00936773.
 XX
 PR 30-JUL-1997; 97US-0054209P.
 PR 30-JUL-1997; 97US-0054211P.
 PR 30-JUL-1997; 97US-0054212P.
 PR 30-JUL-1997; 97US-0054213P.
 PR 30-JUL-1997; 97US-0054214P.
 PR 30-JUL-1997; 97US-0054215P.
 PR 30-JUL-1997; 97US-0054217P.
 PR 30-JUL-1997; 97US-0054218P.
 PR 30-JUL-1997; 97US-0054236P.
 PR 30-JUL-1997; 97US-0054236P.
 PR 18-AUG-1997; 97US-0055968P.
 PR 18-AUG-1997; 97US-0055969P.
 PR 18-AUG-1997; 97US-0055972P.
 PR 18-AUG-1997; 97US-0056534P.
 PR 19-AUG-1997; 97US-0056543P.
 PR 19-AUG-1997; 97US-0056543P.
 PR 19-AUG-1997; 97US-0056543P.
 PR 19-AUG-1997; 97US-0056727P.
 PR 19-AUG-1997; 97US-0056729P.
 PR 19-AUG-1997; 97US-0056730P.
 PR 19-AUG-1997; 97US-0056730P.
 PR 26-JAN-1999; 99US-00236557.
 PR 21-SEP-2000; 2000US-0066984.
 PR 30-MAR-2001; 2001US-00820649.
 PR 05-JUN-2001; 2001US-0295558P.
 PR 04-JUN-2002; 2002US-00160162.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Feng P, Lafleur DW, Moore PA, Shi Y, Kyaw H, Li Y,
 PI Zeng Z, Carter KC, Endress GA, Wei Y, Fan P, Rosen CA,
 XX
 DR WPI: 2005-161941/17.
 DR P-PSDB; ADY25460.
 PT New nucleic acid molecule encoding human secreted protein, useful for

cytostatic; neoplasm; gene; ss.
 Homo sapiens.
 MO2005049806-A2.
 02-JUN-2005.
 11-MAR-2004; 2004WO-US007412.
 14-MAR-2003; 2003US-00389559.
 (NUVE-) NUVELO INC.
 Tang Y, Wang J, Wang ZW, Zhang J, Ren F, Zhou P, Ma Y;
 Ghosh M, Xue A, Aundi V, Zhao Q, Wang D, Goodrich R, Chen R;
 Wehrman T, Meng G, Boyle B;
 WPI; 2005-417730/42.
 P-PSDB; AEA20104.
 New polynucleotide encoding a polypeptide with biological activity,
 useful for treating a disease or disorder, e.g. osteoarthritis, burns,
 infection, or cancer.
 Claim 1. SEQ ID NO 231; 500bp; English.
 The invention describes a new isolated polynucleotide (1) encoding a
 polypeptide with biological activity comprising: a nucleotide sequence of
 SEQ ID NOS: 1-567 (fully defined); a nucleotide sequence that hybridizes
 to the sequence of (1) under stringent hybridization conditions; or a
 nucleotide sequence having greater than 99% sequence identity with the
 sequence of (1). Also described are: a(n) (expression) vector comprising
 (1); a host cell genetically engineered to comprise (1) operatively,
 associated with a regulatory sequence that modulates expression of the
 polynucleotide in the host cell; an isolated polypeptide comprising a
 sequence of SEQ ID NOS: 568-1134 (fully defined), where the polypeptide
 is: a polypeptide encoded by (1); or a polypeptide encoded by a
 polynucleotide hybridizing under stringent conditions with any one of SEQ
 ID NOS: 1-567; a composition comprising the polypeptide of (3) and a
 carrier; an antibody directed against the polypeptide of (3); a method
 for detecting (1) in a sample; a method for detecting the polypeptide of
 (3) in a sample; a method for identifying a compound that binds to the
 polypeptide of (3); a method for producing the polypeptide of (3); and a
 collection of polynucleotides, where the collection comprising of at
 least one of SEQ ID NOS: 1-567. (1) is a polynucleotide comprising any of
 the sequences of SEQ ID NOS: 1-567 encoding a polypeptide with biological
 activity, which comprises any of the amino acid sequence of SEQ ID NOS:
 568-1134. All sequences are useful in diagnostics, forensic, and gene
 mapping, in identifying of mutations responsible for genetic disorders or
 other traits, in assessing biodiversity, and for producing many other
 types of data and products dependent on DNA and amino acid sequences. The
 e.g. osteoporosis, osteoarthritis, periodontal disease, burns, CNS and
 peripheral disease, Alzheimer's disease, Parkinson's disease, stroke,
 autoimmune disorders, viral infection, or cancer. This sequence encodes a
 novel polypeptide of the invention.
 SEQ Sequence 450 BP; 66 A; 180 C; 157 G; 47 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 4.75e-26 Length: 450
 Score: 253.50 Matches: 50
 Percent Similarity: 76.9% Conservative: 10
 Best Local Similarity: 64.1% Mismatches: 13
 Query Match: 56.0% Indels: 5
 DB: 14 Gaps: 2
 US-10-071-645-2 (1-85) x AEA19537 (1-450)
 QY 1 MetTGTGUAValLeuProTyrGlyAspGlnLysLeuSerProTyrGly-----Asp 17

DB 36 ATGCCAGATCTCTCCCTACAGCAAGATGCGCCGCTCGCCAGACCCCGAG 95
 QY 18 G1yG1yAspValG1yG1n1LePheSerCySArgLeuG1nAPTranAenPheNegly 37
 DB 96 GGCTCCGACCTCTCC-----TTGAGTCCCGCTCGAGGACACMACCTCTCTTCGCG 149
 QY 38 A1aG1yG1nAsnLysArgProTyrG1yG1n1Leg1yAysSerLysArgVal1a1 57
 DB 150 GGCAACGAGCCGACGACCCCGGAGCTGGGCGAGATCGGCGGAGGAGGAGGAGG 209
 QY 58 I1eG1yAspAspArg11eAspAspVal1eLysAsnMetThraPysA1aPro 75
 DB 210 ATCGAGATGACCGGATGACGACGCTCTGAGGGAGTGGGAGGAGGAGGAGG 263
 RESULT 15
 ID ABRK1646 standard; cDNA, 550 BP.
 AC ABRK1646;
 XC
 XN 05-JUN-2002 (first entry)
 DE Human cDNA encoding calmodulin-dependent protein kinase inhibitor.
 KW Human; ss; gene; Cam-KIIN; calmodulin-dependent protein kinase inhibitor;
 KW treating stroke; head trauma; multiple sclerosis; Parkinson's disease;
 KW Alzheimer's disease; spinal cord injury; mental disorder; memory deficit;
 KW epilepsy; schizophrenia; bipolar disorder; cancer; ischaemia;
 KW lung disorder; malfunction of secretion; pancreatic disease; pain;
 KW immune system disorder; vaccine; gene therapy; chromosome 3;
 KW hereditary spastic paraplegia.
 XX
 OS Homo sapiens.
 FH
 FT Key Location/Qualifiers
 FT CDS 134..373
 FT /tag= "a
 FT /product= "Cam-KIIN"
 XX
 XX MO200216415-A2.
 XX
 XX 28-FEB-2002.
 XX
 XX 23-AUG-2001; 2001WO-EP009748.
 XX
 XX 25-AUG-2000; 2000EP-00118541.
 XX
 XX (MERE) MERCK PATENT GMEH.
 XX
 XX Duecker K;
 XX
 XX WPI; 2002-280911/32.
 XX P-PSDB; AAU77100.
 XX
 XX Novel calmodulin-dependent protein kinase inhibitor polypeptides useful
 XX for treating stroke, trauma, multiple sclerosis, Parkinson's disease,
 XX Alzheimer's disease, spinal cord injury, mental disorders, memory
 XX disorders.
 XX
 XX Claim 4; Page 33; 34pp; English.
 XX
 XX The invention relates to an isolated calmodulin-dependent protein kinase
 XX inhibitor (Cam-KIIN) and its encoding polynucleotide, variants and
 XX fragments. Also included are an expression system comprising a
 XX polynucleotide capable of producing Cam-KIIN, when the expression vector
 XX is present in a compatible host cell, producing Cam-KIIN, comprising
 XX culturing the cell under expression conditions, and recovering the
 XX polypeptide, a fusion protein consisting of the immunoglobulin Fc-region
 XX and Cam-KIIN, an anti Cam-KIIN antibody and screening for identifying
 XX compounds that stimulate or inhibit the function or level of Cam-KIIN.
 XX Cam-KIIN and the polynucleotide are useful for treating stroke, head
 XX trauma, multiple sclerosis, Parkinson's disease, Alzheimer's disease,

CC spinal cord injury, mental disorders, memory deficits, epilepsy,
 CC schizoprenia, bipolar disorders, cancers, ischemic conditions of the
 CC heart, lung disorders caused by malfunctioning of secretion, diseases
 CC caused by disturbed pancreas secretion behaviour, pain, and disorders of
 CC immune system. Cam-KiIN and the polynucleotide are also useful as
 CC vaccines for inducing immunological response in a mammal. Cam-KiIN is
 CC useful in disease diagnosis and in assays for screening agonistic or
 CC antagonistic compounds. Cam-KiIN is also useful for identifying membrane
 CC bound or soluble receptors. The polynucleotide is useful as diagnostic
 CC reagent for detecting mutations in the associated gene, in the
 CC recombinant production of Cam-KiIN, for chromosome localization studies,
 CC as a valuable tool in tissue expression studies, and in gene therapy. The
 CC antibody is useful for isolating and identifying clones expressing Cam-
 CC KiIN, and for purifying Cam-KiIN. The gene for Cam-KiIN is located on
 CC human chromosome 3 in a region associated with hereditary spastic
 CC paraplegia. The present sequence is the cDNA encoding human Cam-KiIN
 XX

XX Sequence 550 BP; 77 A; 225 C; 187 G; 61 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6,19e-26 Length: 550
 Score: 253.50 Matches: 50
 Percent Similarity: 76.9% Conservative: 10
 Best Local Similarity: 64.1% Mismatches: 13
 Query Match: 56.0% Indels: 5
 DB: 6 Gaps: 2

US-10-071-645-2 (1-85) x ABK11646 (1-550)

Qy 1 MetTpgIuValIeuProTyrgIyAspGluIyIeuSerProTyrgIy-----Aap 17
 Db 134 ATGTCCAGAGATCTCGCTTCACAGACAGACAGATGCGCGCTTCGCGCAGACCCGAG 193
 Qy 18 GlyGlyAspValGlyGlnIlePheSerCysArgIeuGlnAspThrAspAspPheGly 37
 Db 194 GGTCTCCAGCTCTCC-----TTCACTGCTCCGCTCTGAGAGACACACATCTCTTTCGCG 247
 Qy 38 AlaGlyIleAsnIyAspProTyrgIyIeuGlnIleGlyArgSerIyAspValVal 57
 Db 248 GGCAACCGGCGAGCGACCCCGCAAGCTGAGGCGAGTCCGCGAGCCAGCGAGTGTG 307
 Qy 58 IlegIuAspAspArgIleAspAspValIeuIyAspMetThrAspIyAlaPro 75
 Db 308 ATCGAGATGACCGAGACACAGCTGAGAGGAGATGAGGAGAGACCGCGCG 361

Search completed: March 9, 2006, 00:06:49
 Job time : 466 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_p2n model

Run on: March 8, 2006, 23:10:05 ; Search time 2337 Seconds
(without alignments)
2067.477 Million cell updates/sec

Title: US-10-071-645-2
Perfect score: 453
Sequence: 1 MWEVLPYGDREKLSPYGDGD.....VLKNTDRAPIVNSPKTMS 85

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=GenEmbl -QFMT=faeap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
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-USER=US10071645 @CGN 1.1 7415 @runat_08032006_115121_4611 -NCPU=6 -ICPU=3
-NO MAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -IONLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DRPOP=6 -DELEXT=7

Database :

GenEmbl:1*
1: gb ba:*
2: gb in:*
3: gb env:*
4: gb om:*
5: gb ov:*
6: gb pat:*
7: gb ph:*
8: gb dr:*
9: gb ro:*
10: gb str:*
11: gb sy:*
12: gb un:*
13: gb vl:*
14: gb hg:*
15: gb pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	453	100.0	1104	AX451459 Sequence
2	413	91.2	860	AY204901 Homo sapi
3	413	91.2	1581	BD276315 MOLECULES

4	413	91.2	1581	6	AX049462	AX049462 Sequence
5	413	91.2	1876	6	AR454597	AR454597 Sequence
6	396	87.4	1592	9	AY523601	AY523601 Mus muscu
7	392	86.5	409	9	AF271156	AF271156 Rattus no
8	391	86.3	237	6	CQ727202	CQ727202 Sequence
9	291.5	64.3	3745	5	BC061942	BC061942 xenopus 1
10	290	64.0	3189	6	AX451461	AX451461 Sequence
11	290	64.0	195076	8	AL391357	AL391357 Human DNA
12	285	62.9	248478	14	AC107845	AC107845 Mus muscu
13	285	62.9	248478	14	AL807249	AL807249 Mouse DNA
14	285	62.9	259224	14	AC109006	AC109006 Rattus no
15	277.5	61.3	2133	5	BC095218	BC095218 Dantio rer
16	273.5	60.4	695	5	CR407503	CR407503 Gallus ga
17	270.5	59.7	1740	5	BC075931	BC075931 Dantio rer
18	259.5	57.3	347	9	AF041854	AF041854 Rattus no
19	253.5	56.0	550	6	BD030206	BD030206 Sequence
20	241	53.2	183	6	BD030206	BD030206 Sequence
21	241	53.2	183	6	AX894673	AX894673 Sequence
22	225	44.9	193826	14	CR558302	CR558302 Homo sapi
23	203.5	44.9	193826	14	CR558302	CR558302 Dantio rer
24	196.5	43.4	162087	5	EX649599	EX649599 zebrafish
25	186.5	43.4	165933	14	CT025582	CT025582 Dantio rer
26	180.5	39.8	195966	9	AC087898	AC087898 Mus muscu
27	180.5	39.8	219564	14	AC073708	AC073708 Mus muscu
28	180.5	39.8	231741	14	AC110855	AC110855 Rattus no
29	180.5	39.8	250010	14	AC074027	AC074027 Mus muscu
30	174.5	38.5	152823	14	AC024530	AC024530 Homo sapi
31	174.5	38.5	166704	8	AC078797	AC078797 Homo sapi
32	174.5	38.5	170400	14	AC048331	AC048331 Homo sapi
33	172	38.0	1321	6	CQ776764	CQ776764 Sequence
34	170.5	37.6	144722	14	AC163964	AC163964 Loxodonta
35	154.5	34.1	146422	5	CR762407	CR762407 zebrafish
36	154.5	34.1	190747	14	BX927120	BX927120 Dantio rer
37	154.5	34.1	192644	14	CR762383	CR762383 Dantio rer
38	133.5	29.5	126141	14	AL356300	AL356300 Homo sapi
39	133.5	29.5	153801	14	AC025224	AC025224 Homo sapi
40	133	29.4	167801	8	BC020630	BC020630 Homo sapi
41	111.5	24.6	315	6	BD119214	BD119214 EST and e
42	111.5	24.6	315	6	AR423661	AR423661 Sequence
43	111.5	24.6	315	6	AX984355	AX984355 Sequence
44	94	20.8	65	6	CO535096	CO535096 Sequence
45	86.5	19.1	50829	8	AC061705	AC061705 Homo sapi

ALIGNMENTS

RESULT 1	AX451459	1104 bp	DNA	linear	PAT 03-JUL-2002
LOCUS	AX451459	Sequence 1 from Patent WO0212279.			
DEFINITION	AX451459				
ACCESSION	AX451459				
VERSION	AX451459.1	GI:21698460			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Homidae; Homo.				
REFERENCE					
AUTHORS	Bihain, B., Bour, B. and Bougueleret, L.				
TITLE	Schizophrenia related gene and protein				
JOURNAL	Patent: WO 0212279-A 1 14-FEB-2002;				
GENSET (FR)					
FEATURES					
source	1..1104				
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	/mol_type="unassigned DNA"				
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	87..344				
	/note="unassigned protein product"				
	/codon_start=1				
	/protein_id="CAD37813.1"				
	/db_xref="GI:21698461"				


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US-10-071-645-2 (1-85) x BD276315 (1-1581)

QY 1 MetTpglUValleuProTyrGlyAspGlyValAspGlyValAsp 20
DB 39 ATGTGGAGGGGCGCCCTACGGCGACGAGAGCTGAGCCCTACGGCGACGCGCGAC 98
QY 21 ValGlyGlnIlePheSerCysArgLeuGlnAspThrAsnAspPheGlyValGlyGln 40
DB 99 GTGGGCGAGATCTTCTCTGCGCCCTGCGAGGACCAACAACCTTCTGCGCGCGCGAG 158
QY 41 AsnLysArgProProlYsLeuGlnIleGlyArgSerIysArgValIleGlyAsp 60
DB 159 AACAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 218
QY 61 AsparGlyIleAspAspValleuLysAsnMetThrAspLysAlaPro-LeuValIserAsn 80
DB 219 GATAGGATGATGACGCTGCTGAAAATATGACGACCAAGCAAGCACTCTGCTGCTACTC 278

RESULT 4
LOCUS AX049462 1581 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 1 from Patent WO0070036.
ACCESSION AX049462.1 GI:12226181
VERSION AX049462.1
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
1 Kaser,M.R., Lai,P., Yue,H., Tang,Y.T., Baughn,M.R. and Azimzal,Y.
Genes expressed in hippocampus
Patent: WO 0070036-A 1 23-NOV-2000;
JOURNAL Incyte Genomics, Inc. (US)
FEATURES
source 1. 1581
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="Incyte ID No.: 239240"

ORIGIN
Alignment Scores:
Pred. No.: 2,1e-40 Length: 1581
Score: 413.00 Matches: 84
Percent Similarity: 96.6% Conservative: 0
Best Local Similarity: 96.6% Mismatches: 1
Query Match: 91.2% Indels: 2
DB: Gaps: 0

US-10-071-645-2 (1-85) x AX049462 (1-1581)

QY 1 MetTpglUValleuProTyrGlyAspGlyValAspGlyValAsp 20
DB 39 ATGTGGAGGGGCGCCCTACGGCGACGAGAGCTGAGCCCTACGGCGACGCGCGAC 98
QY 21 ValGlyGlnIlePheSerCysArgLeuGlnAspThrAsnAspPheGlyValGlyGln 40
DB 99 GTGGGCGAGATCTTCTCTGCGCCCTGCGAGGACCAACAACCTTCTGCGCGCGCGAG 158
QY 41 AsnLysArgProProlYsLeuGlnIleGlyArgSerIysArgValIleGlyAsp 60
DB 159 AACAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 218
QY 61 AsparGlyIleAspAspValleuLysAsnMetThrAspLysAlaPro-LeuValIserAsn 80
DB 219 GATAGGATGATGACGCTGCTGAAAATATGACGACCAAGCAAGCACTCTGCTGCTACTC 278

ORIGIN
Alignment Scores:
Pred. No.: 2,53e-40 Length: 1876
Score: 413.00 Matches: 84
Percent Similarity: 96.6% Conservative: 0
Best Local Similarity: 96.6% Mismatches: 1
Query Match: 91.2% Indels: 2
DB: Gaps: 0

US-10-071-645-2 (1-85) x AR454597 (1-1876)

QY 1 MetTpglUValleuProTyrGlyAspGlyValAspGlyValAsp 20
DB 355 ATGTGGAGGGGCGCCCTACGGCGACGAGAGCTGAGCCCTACGGCGACGCGCGAC 414
QY 21 ValGlyGlnIlePheSerCysArgLeuGlnAspThrAsnAspPheGlyValGlyGln 40
DB 415 GTGGGCGAGATCTTCTCTGCGCCCTGCGAGGACCAACAACCTTCTGCGCGCGCGAG 474
QY 41 AsnLysArgProProlYsLeuGlnIleGlyArgSerIysArgValIleGlyAsp 60
DB 475 AACAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 534
QY 61 AsparGlyIleAspAspValleuLysAsnMetThrAspLysAlaPro-LeuValIserAsn 80
DB 535 GATAGGATGATGACGCTGCTGAAAATATGACGACCAAGCAAGCACTCTGCTGCTACTC 594
QY 80 T-ProlyserTherMetSer 85
DB: 595 CCCCAAGACATAGT 611

RESULT 6
LOCUS AY523601 1592 bp mRNA linear ROD 04-FEB-2004
DEFINITION Mus musculus CamkII inhibitor protein alpha mRNA, complete cds.
ACCESSION AY523601
VERSION AY523601.1 GI:41393698
KEYWORDS Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.

REFERENCE
1 Sougata,S. and Rangarajan,P.N.
Identification and characterization of mouse CamkII inhibitor alpha
(CamkII-alpha) from mouse brain
JOURNAL Unpublished

```

REFERENCE 2 (bases 1 to 1592)
 AUTHORS Sougata, S. and Rangarajan, P. N.
 TITLE Direct Submission
 JOURNAL Submitted (10-JAN-2004) Biochemistry, Indian Institute of science,
 C V Raman Avenue, Bangalore, Karnataka 560012, India
 LOCATION/Qualifiers

FEATURES
 source
 1..1592
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="Swiss"
 /db_xref="taxon:10090"
 /chromosome="4"
 1..237
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 /codon_start=1
 /product="CamKII inhibitor protein alpha"
 /protein_id="AA02090.1"
 /db_xref="GI:41393699"
 /translation="MSRVLPYGDGKSPYGGDGVGQIFSCRLQDTNNPFGAGSKRP
 PKLGQIGRSKRVIEDRIDVLTMTDKAPPGV"

CDS
 1..237
 /note="inhibitor protein for CamKII β ; CamKII α -alpha"
 /codon_start=1
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 /protein_id="AA02090.1"
 /db_xref="GI:41393699"
 /translation="MSRVLPYGDGKSPYGGDGVGQIFSCRLQDTNNPFGAGSKRP
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ORIGIN

Alignment Scores:
 Pred. No.: 2,5e-38 Length: 1592
 Score: 396.00 Matches: 78
 Percent Similarity: 95.2% Conservative: 1
 Best Local Similarity: 94.0% Mismatches: 3
 Query Match: 87.4% Indels: 1
 DB: 9 Gaps: 0

US-10-071-645-2 (1-85) x AVS23601 (1-1592)

QY 1 MetTPGluValLeuProTYGlyAspGluYLeuSerProTYGlyAspGlyGlyAsp 20
 Db 1 ATGTGGAGGAGTGTGCTTACGCGACGAGAAAGCTGAGCCCTACGCGGACGCGGAC 60
 QY 21 ValGlyGlnIlePheSerCysArgLeuGlnAspThrAsnAspPheGlyValGlyGln 40
 Db 61 GTGGGCCAGATCTTCTGTCGCGCTGCGAGACCAACAATCTTCTGCGGCGTGGCAG 120
 QY 41 AsnLYsArgProProLYsLeuGlyGlnIleGlyArgSerLYsArgValIleGlyAsp 60
 Db 121 AGCAAGCGGCGCTCCGAGCTGGCCGAGATCGCGGAGCAAGGCGTGTATTGAAGAT 180
 QY 61 AspArgIleAspAspValIleuLYsAsnMetThrAspLYsAla-ProLeuValSerAsn 80
 Db 181 GATAGGATGATGACGTGCTGAACCATGACCGACCAAGGACCCCTGATGCTAACTG 240
 QY 80 rProLYs 82
 Db 241 CCCCAA 247

RESULT 7
 AF271156 409 bp mRNA linear ROD 29-OCT-2001
 LOCUS AF271156
 DEFINITION Rattus norvegicus Cam-kinase II inhibitor alpha mRNA, complete cds.
 ACCESSION AF271156
 VERSION AF271156.1 GI:8453199
 KEYWORDS
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Rattus.
 1 (bases 1 to 409)
 Chang, B.H., Mukherji, S. and Soderling, T.R.
 Calcium/calmodulin-dependent protein kinase II inhibitor protein:
 localization of isoforms in rat brain
 Neuroscience 102 (4), 767-777 (2001)
 1192241
 2 (bases 1 to 409)
 Chang, B.H., Mukherji, S. and Soderling, T.R.
 Direct Submission

JOURNAL Submitted (23-MAY-2000) Vollum, OHSU, 3181 SW Sam Jackson Park
 Road, Portland, OR 97201, USA
 LOCATION/Qualifiers

FEATURES
 source
 1..409
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 10..246
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CDS
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ORIGIN

Alignment Scores:
 Pred. No.: 1,71e-38 Length: 409
 Score: 392.00 Matches: 77
 Percent Similarity: 95.2% Conservative: 2
 Best Local Similarity: 92.8% Mismatches: 3
 Query Match: 86.5% Indels: 1
 DB: 9 Gaps: 0

US-10-071-645-2 (1-85) x AF271156 (1-409)

QY 1 MetTPGluValLeuProTYGlyAspGluYLeuSerProTYGlyAspGlyGlyAsp 20
 Db 10 ATGTGGAGGAGTGTGCTTACGCGACGAGAAAGCTGAGCCCTACGCGGACGCGGAC 69
 QY 21 ValGlyGlnIlePheSerCysArgLeuGlnAspThrAsnAspPheGlyValGlyGln 40
 Db 70 GTGGGCCAGATCTTCTGTCGCGCTGCGAGACCAACAATCTTCTGCGGCGTGGCAG 129
 QY 41 AsnLYsArgProProLYsLeuGlyGlnIleGlyArgSerLYsArgValIleGlyAsp 60
 Db 130 AGCAAGCGGCGCTCCGAGCTGGCCGAGATCGCGGAGCAAGGCGTGTATTGAAGAT 189
 QY 61 AspArgIleAspAspValIleuLYsAsnMetThrAspLYsAlaPro-LeuValSerAsn 80
 Db 190 GATAGGATGATGACGTGCTGAACCATGACCGACCAAGGACCACTCTGCTAACTG 249
 QY 80 rProLYs 82
 Db 250 CCCCAA 256

RESULT 8
 CO272702 237 bp DNA linear PAT 03-FEB-2004
 LOCUS CO272702
 DEFINITION Sequence 13136 from Patent WO02068579.
 ACCESSION CO272702
 VERSION CO272702.1 GI:4292526
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1
 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
 Kits, such as nucleic acid arrays, comprising a majority of
 humanexons or transcripts, for detecting expression and other uses
 thereof: WO 02068579-A 13136 06-SEP-2002;
 Patent: WO 02068579-A 13136 06-SEP-2002;
 Location/Qualifiers
 1..237
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FEATURES
 source
 1..237
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 /db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.:	1.24e-38	Length:	237
Score:	391.00	Matches:	74
Percent Similarity:	98.7%	Conservative:	0
Best Local Similarity:	98.7%	Mismatches:	1
Query Match:	86.3%	Indels:	0
DB:	6	Gaps:	0

US-10-071-645-2 (1-85) x CQ727202 (1-237)

QY 1 MetTPGluValleuProTyGlyAspGluLeuSerProTyGlyAspGlyValAsp 20

DB 1 ATGTGGAGGGGCTGCTGCTTACCGACAGAGAGCTGAGCCCTACGGCGAGCGGGCGAC 60

QY 21 ValGlyGlnIlePheSerCysArgLeuGlnAspThrAsnAspPheGlyValGlyGln 40

DB 61 GTGGGCGAGATCTTCTCTCCGCCCTGCGAGGACCAACACTTCTTCCGGCGGGCGAG 120

QY 41 AsnYAspArgProPheProTyLeuGlyGlnIleGlyArgSerIleArgValIleGlyAsp 60

DB 121 AACAAAGGGGCGGCGCAAGCTGGGCGAGATCGCGCGGAGCAAGCGGCTTGTATTGAAGAT 180

QY 61 AspArgIleAspAspValleuAspAspMetThrAspIleValAsp 75

DB 181 GATGAGATGATGATCTGCTGAAAATATGACCAAGGCACT 225

RESULT 9

LOCUS BC061942 3745 bp mRNA linear VRT 12-NOV-2003

DEFINITION Xenopus laevis cDNA clone MGC:68568 IMAGE:403155, complete cds.

ACCESSION BC061942 GI:38303924

VERSION MGC.

KEYWORDS Xenopus laevis (African clawed frog)

SOURCE Xenopus laevis

ORGANISM Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumetazoa; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.

1 (bases 1 to 3745)

REFERENCE 1 Klein, S.L., Straubeberg, R.L., Wagner, L., Pontius, J., Clifton, S.W. and Richardson, P. Genetic and genomic tools for Xenopus research: The NIH Xenopus Initiative

TITLE Dev. Dyn. 225 (4), 384-391 (2002)

JOURNAL PUBMED 12454917

REFERENCE 2 (bases 1 to 3745)

AUTHORS Straubeberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shemmer, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.W., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Lounellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hally, S.W., Villalón, D.R., Muzny, D.M., Sodergren, E.J., Du, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, J., Whiting, M., Madan, A., Young, A.C., Shcherbakov, Y., Dickerson, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Gittum, J., Schmitt, J., Myers, R.M., Butcherfield, Y.S., Krzyzanski, M.T., Skalska, U., Smalins, D.E., Scherch, A., Schein, J.E., Jones, S.V. and Matra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE 12477932

JOURNAL 3 (bases 1 to 3745)

PUBMED Klein, S. and Straubeberg, R.

REFERENCE Direct Submission

AUTHORS Submitted (10-NOV-2003) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human

REMARK

COMMENT

Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD 20852-7510, USA

NIH-MGC Project

Contact: XGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Igor David

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)

Sequencing Center (NISC),

Gatthersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc.mgc@nrci.nih.gov

Akhter, N., Ayala, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakeley, R.W., Bouffard, G.G., Breen, K., Brickley, C., Brooker, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Maduro, O.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantrop, S., Thomas, P.J., Touchman, J.W., Taurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at: <http://image.llnl.gov>

Series: IRAX Plate: 128 Row: I Column: 7

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

Location/Qualifiers

1. 3745

/organism="Xenopus laevis"

/mol_type="mRNA"

/db_xref="taxon:8355"

/clone="MGC:68568 IMAGE:4031555"

/tissue_type="Kidney, adult Xenopus"

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/lab_host="DH10B"

/note="Vector: pCWT-SPORT6"

173. 412

/product="unknown (protein for MGC:68568)"

/protein_id="AA61942.1"

/db_xref="GI:38303925"

/translation="MSEILPYDEDMGHGSDGVGQISFSCRLQDTSPPFGNQQR PPKLQIGRAKRVVIDRIDEVLKGVSDKSPSGV"

ORIGIN

Alignment Scores:

Pred. No.:	3.53e-25	Length:	3745
Score:	291.50	Matches:	55
Percent Similarity:	85.5%	Conservative:	10
Best Local Similarity:	72.4%	Mismatches:	1
Query Match:	64.3%	Indels:	1
DB:	5	Gaps:	1

US-10-071-645-2 (1-85) x BC061942 (1-3745)

QY 1 MetTPGluValleuProTyGlyAspGluLeuSerProTyGlyAspGlyValAsp 20

DB 173 ATGTGGAGGGGCTGCTGCTTACCGACAGAGAGCTGAGCCCTACGGCGAGCGGGCGAC 232

QY 21 ValGlyGlnIlePheSerCysArgLeuGlnAspThrAsnAspPheGlyValGlyGln 39

DB 233 GTGGGCGAGATCTTCTCTCCGCCCTGCGAGGACCAACACTTCTTCCGGCGGGCGAG 292

QY 40 GlnAsnYAspArgProPheProTyLeuGlyGlnIleGlyArgSerIleArgValIleGlyAsp 59

DB 293 CAGCGAGAAAAGACCCCAACCTGGGCGAGATGGAGAGCCCAAGAGAGCTTGTATTGAAG 352

QY 60 AspAspArgIleAspAspValleuAspAspMetThrAspIleValAsp 75

DB 353 GATGAGATGATGATCTGCTGAAAATATGACCAAGGCACT 400

```

RESULT 10
AX451461          3189 bp      DNA      linear      PAT 03-JUL-2002
LOCUS             AX451461
DEFINITION        Sequence 3 from Patent WO0212279.
ACCESSION         AX451461
VERSION           AX451461.1 GI:21698462
KEYWORDS
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 Bihain, B., Bour, B. and Bougueleret, L.
Schizophrenia related gene and protein
Patent: WO 0212279-A 3 14-FEB-2002;
JOURNAL
GENSET (FR)
FEATURES
source            Location/Qualifiers
1..3189
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Prod. No.:         4.5e-25      Length:      3189
Score:             290.00      Matches:     54
Percent Similarity: 98.2%      Conservative: 0
Best Local Similarity: 98.2%   Mismatches:  1
Query Match:       64.0%      Indels:      0
DB:                Gaps:      0
US-10-071-645-2 (1-85) x AX451461 (1-3189)
QY                1 MetTgPiValIeudProTyRqLYaSPqULyLSeuSerProTyRqLYaSPqLYqLYaSP 20
Db                499 ATGTGGAGGGTGGCGCCCTACCGGACGAGAGCTGAGCCCTACGCGGACGCGGGCGAGC 558
QY                21 VALGIYnIIePheSerCYaRgLeuGlnAaPThraNaAaPheGlyYAlaGIyGln 40
Db                559 GTGGGCGAGATCTTCTCCGCGCTGCGACGACCAACACTTCTTGGGGCGCGGCGAG 618
QY                41 AaNYaARgProPProLYaLeuGlyGlnIIeGlyYARgSerLYaRg 55
Db                619 AACAGCGCGCGCGCCCAAGCTGGGGCCAGATCCGCGCGGACAGCGG 663
RESULT 11
AL391357/c        195076 bp      DNA      linear      PRI 18-MAY-2005
LOCUS             AL391357/c
DEFINITION        Human DNA sequence from clone RP11-401M16 on chromosome 1 Contains
the gene for calcium/calmodulin-dependent protein kinase II
(CaMKIIA1alpha), the gene for a novel protein (FLJ12875), a
ribosomal protein S4 X-linked (RPS4X) pseudogene, the CNA gene for
cytidine deaminase, the PINK1 gene for PTEN induced putative kinase
1, a novel gene (FLJ00387), the DOST gene for
dolichyl-diphosphooligosaccharide-protein glycosyltransferase and
the 3' end of the KIF17 gene for kinesin family member 17, complete
sequence.
ACCESSION         AL391357
VERSION           AL391357.20 GI:16501137
KEYWORDS          HTG; CaMKIIA1alpha; CDA; cytidine deaminase; DOST; FLJ00387;
FLJ12875; KIF17; PINK1; RPS4X.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 195076)
Kimberley, A.
Direct Submission
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk

```

COMMENT

On Oct 26, 2001 this sequence version replaced gi:16304938.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1> RP11-401M16 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.choi.org/bacpac/home.htm> VECTOR: pBAC3.6

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: vegas@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

FEATURES

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source            Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
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/clone_id="RP11-401M16"
1
/note="Clone left end: RP11-401M16"
misc_feature      complement(join(4198..5526,7021..8027))
gene              /gene="RP11-401M16.1"
locus_tag="RP11-401M16.1-001"
complement(join(4198..5526,7021..8027))
mRNA              /gene="RP11-401M16.1"
locus_tag="RP11-401M16.1-001"
product="calcium/calmodulin-dependent protein kinase II (CaMKIIA1alpha)"
/note="match: cDNAs: Em:AF116637.1 Em:AY204901.1"
complement(4198)
polyA_site        /gene="RP11-401M16.1"
locus_tag="RP11-401M16.1-001"
complement(4218..4223)
polyA_signal      /gene="RP11-401M16.1"
locus_tag="RP11-401M16.1-001"
complement(join(4994..5526,6174..6452))
gene              /gene="RP11-401M16.1"
locus_tag="RP11-401M16.1-002"
complement(join(4994..5526,6174..6452))
mRNA              /gene="RP11-401M16.1"
locus_tag="RP11-401M16.1-002"
product="calcium/calmodulin-dependent protein kinase II (CaMKIIA1alpha)"
/note="match: ESTs: Em:AL536560.2"
complement(join(5456..5526,7021..7186))
CDS               /gene="RP11-401M16.1"
locus_tag="RP11-401M16.1-001"
/standard_name="OTTHUMP0000002879"
/note="match: proteins: Tr:AA049802 Tr:Q9U115"
codon_start=1
product="calcium/calmodulin-dependent protein kinase II (CaMKIIA1alpha)"
protein_id="CAH73469.1"
/db_xref="GI:55664520"
/db_xref="GOA:Q7Z7J9"
/db_xref="UniProt/TrEMBL:Q7Z7J9"

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misc_feature
/note="Clone_right_end: RP4-749H3"
complement (21255)
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/locus_tag="RP11-401M16.2-001"
complement(join(21257..23226,23876..23996,25029..25116,29712..29968))
/gene="RP11-401M16.2"
/locus_tag="RP11-401M16.2-001"
/locus_tag="RP11-401M16.2-001"
/note="match: CDNA: Em:AB097015.1 Em:AK022937.1 Em:AL83389.1 Em:BC010101.1 Em:BC010101.2 Em:BC014010.1"
complement(21269..21274)
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/locus_tag="RP11-401M16.2-001"
complement(join(22497..23226,23876..23996,25029..25116,29712..29968))
/gene="RP11-401M16.2"
/locus_tag="RP11-401M16.2-001"
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/note="match: protein: Tr:BC77368 Tr:Q8BHF2 Tr:Q8VCH5 Tr:Q969V5 Tr:Q9DCV9 Tr:Q9H9B5"
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/db_xref="GI:55664521"
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/db_xref="InterPro:IPR001841"
/db_xref="UniProt/TREMBL:Q969V5"
/translation="MESGRPSLCPIQLGTSVVTALYSVYRKQAVSGLKGAKK VHLGDKLSIEAKGKCVAVIAGVAVSEVETLNSQFENCKGVQLQLTLOEKRY MNRTTLMNDCSIHORVTVPFDLVPEEDVAVARVAKPDSVDLGLVEYKRY PSIOSPTDVIQHYISGRPKIOETEMKAGATLGVGLVDNNSVALQPPQGMQ VYLSQDPDSLQROESSVRLMVLVAGFATCATLFTLRKOYLOEROERLRLKQMG EEFQEHQAQLSRAPEDRESLKSACVCLSSFFKSCVFLCGHVCSCTECYRALPEBK KCPICROAITRVIPLYNS"
47796..48558
/locus_tag="RP11-401M16.3-001"
/pseudo
47796..48558
/locus_tag="RP11-401M16.3-001"
/note="match: proteins: Sw:P22090 Sw:P47836 Tr:Q62738 Tr:Q62739 Tr:Q801H0 Tr:Q86LM7 Tr:Q86LM8 Tr:Q9TTK5"
/pseudo
/codon_start=1
/product="ribosomal protein S4, X-linked (RPS4X) pseudogene"
47426..76817
/gene="PAM43B"
/locus_tag="RP11-401M16.9-001"
47426..76817
/gene="PAM43B"
/locus_tag="RP11-401M16.9-001"
/product="family with sequence similarity 43, member B"
/note="match: CDNA: Em:AK126900.1"
47481..75770
/gene="PAM43B"
/locus_tag="RP11-401M16.9-001"
/standard_name="OTTHUMP0000063209"
/note="match: proteins: Tr:BAC68742"
/codon_start=1
/product="family with sequence similarity 43, member B"
/protein_id="CAH73473.1"
/db_xref="GI:55664523"
/db_xref="UniProt/Swiss-Prot:Q62752"
/translation="MLPRRNKFLVLEDEAKKAKSLSPGLAVTSLSSPLRSCDPL PDWPLRLGRVRSRROKVELNKEDPTVYVLAAGVTLAKGDCCTDAVGKIMWC GPGGTKMLTLGPHGIRMOFCERSAAGSGGRRAHAYLLPRITCTADAGKIMARC WYVRHQRKAVLRCNAVLLARHAKRLARLRLROTALAFAFDFRLQROSDRAHYR QQLRAGCAASVPRAPLRLNKAACAYPPPSERSGAPRLSSIGEDDEEDDADAE
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75757..75801
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/locus_tag="RP11-401M16.9-001"
/note="Single clone region. Assembly confirmed by restriction digest data."
76793..76798
/gene="PAM43B"
/locus_tag="RP11-401M16.9-001"
76817
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/locus_tag="RP11-401M16.9-001"
108464
/note="Clone Left end: RP11-72P17"
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/gene="CDA"
/locus_tag="RP11-401M16.4-001"
join(11075..111090,126735..126846,135649..135706,140259..140715)
/gene="CDA"
/locus_tag="RP11-401M16.4-001"
/product="cytidine deaminase"
/note="match: CDNA: Em:BC048284.1 Em:BC054036.1 Em:U27943.1 Em:S52873.1"
join(110893..111090,126735..126846,140259..140710)
/gene="CDA"
/locus_tag="RP11-401M16.4-002"
join(110893..111090,126735..126846,140259..140710)
Alignment Scores:
Pred. No.: 4,23e-23 Length: 195076
Score: 290.00 Matches: 54
Percent Similarity: 98.2% Conservative: 0
Best Local Similarity: 98.2% Mismatches: 1
Query Match: 64.0% Indels: 0
DB: 8 Gaps: 0
US-10-071-645-2 (1-85) x AL391357 (1-195076)
QY 1 MetTPGIVAlLeuProTcYgIaSPGLuLyLeuSerProTcYgIaSPGLyGIYaAP 20
DB 7186 ATGTGGAGGAGTGTGCTGCTCAAGCGGACGAGACGTAGCGCCTTAGCGGAGCGGCGAGC 7127
QY 21 ValGlyGlnIlePheSerCyArGylGluGlnAptThrAraAspPheGlyAlaGlyGln 40
DB 7126 GTGGCCAGATCTTCTCCCGCGCTGCGAGGACACACACATCTTCTGCGCGCGGCGAG 7067
QY 41 AanlyAaPpPpPpPpPpPpPpPpPpPpPpPpPpPpPpPpPpPpPpPpPpPpPpPp 55
DB 7066 AACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 7022
RESULT 12
AC107845/c 170878 bp DNA linear HTG 13-MAR-2004
LOCUS AC107845
DEFINITION Mus musculus clone RP23-308C7, WORKING DRAFT SEQUENCE, 24 unordered
pieces.
ACCESSION AC107845
VERSION AC107845.3 GI:45430114
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FUJLTOP.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sclerogonathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE
1 Birren,B., Nussbaum,C. and Lander,E.
Mus musculus, clone RP23-308C7
Unpublished
2 (bases 1 to 170878)
REFERENCE
1 Birren,B., Linton,L., Nussbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barnes,N., Bastien,V., Boguski,J., Boulanger,B.,
Brown,A., Camarata,J., Campiano,A., Chang,J., Chazaro,B.,
```



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gap      43833..43932      /estimated_length=100
misc_feature 43933..48142 /note="assembly_fragment"
gap      48143..48242      /estimated_length=100
misc_feature 48243..48360 /note="assembly_fragment"
gap      48361..48480      /estimated_length=100
misc_feature 48481..48639 /note="assembly_fragment"
gap      48640..48776      /estimated_length=100
misc_feature 48777..49077 /note="assembly_fragment"
gap      49078..49259      /estimated_length=100
misc_feature 49260..49528 /note="assembly_fragment"
gap      49529..49628      /estimated_length=100
misc_feature 49629..49722 /note="assembly_fragment"
gap      49723..49822      /estimated_length=100
misc_feature 49823..49912 /estimated_length=100

Alignment Scores:
Pred. No.: 1,496-22      Length: 170878
Score: 285.00      Matches: 53
Percent Similarity: 98.2%      Conservative: 1
Best Local Similarity: 96.4%      Mismatches: 1
Query Match: 62.9%      Indels: 0
DB: 14      Gaps: 0

US-10-071-645-2 (1-85) x AC107845 (1-170878)
Qy      1 MetTTPGIVaUaLeuProTyTgIYAaPqIuYbLeuSerProTyTgIYAaPqIuYbAaP 20
Db      100243 ATGTGGAAGGCTGCTGCTCAACGGGACGAGAGCTAGCCCTTACGGGACGCGCGGAC 100184
Qy      21 ValGIGVnIlePheSerCyArGLeuGlnAaPThrAaAaPhePheGlyAlaGlyGln 40
Db      100183 GTGGGCGAGATCTTCTGCTGCGGCTGCGAGACCAACACTTCTTGGGGCTGGGCAg 100124
Qy      41 AaMlyAaRProProTyLeuGlyGlnIleGlyAaGSerIyaAaG 55
Db      100123 AGCAAGCGGCTCCCAAGCTGGGCGAGATCGGCGGAGCAAGGCG 100079

RESULT 13
LOCUS      AL807249      248479 bp      DNA      linear      ROD 24-OCT-2002
DEFINITION      Mouse DNA sequence from clone RP23-25C1 on chromosome 4, complete
ACCESSION      AL807249      GI:24395096
VERSION      AL807249.8      GI:24395096
KEYWORDS      HTG.
SOURCE      Mus musculus (house mouse)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Scurionathia; Murioidea; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 248479)
AUTHORS      Blakey,S.

```

```

TITLE      Direct Submission
JOURNAL
COMMENT      Submitted (18-OCT-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Oct 25, 2002 this sequence version replaced gi:2436558.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
-----

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone and more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sw:
SWISSPROT; Tr: TrEMBL; Wp: WormPEP; Information on the WormPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
from the RPI-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBAC3.6.

FEATURES
SOURCE
1..248479
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="4"
/clone="RP23-25C1"
/clone_1fb="RPI-23"

ORIGIN
Alignment Scores:
Pred. No.: 2,256-22      Length: 248479
Score: 285.00      Matches: 53
Percent Similarity: 98.2%      Conservative: 1
Best Local Similarity: 96.4%      Mismatches: 1
Query Match: 62.9%      Indels: 0
DB: 9      Gaps: 0

US-10-071-645-2 (1-85) x AL807249 (1-248479)
Qy      1 MetTTPGIVaUaLeuProTyTgIYAaPqIuYbLeuSerProTyTgIYAaPqIuYbAaP 20
Db      239715 ATGTGGAAGGCTGCTGCTCAACGGGACGAGAGCTAGCCCTTACGGGACGCGCGGAC 239774
Qy      21 ValGIGVnIlePheSerCyArGLeuGlnAaPThrAaAaPhePheGlyAlaGlyGln 40
Db      239775 GTGGGCGAGATCTTCTGCTGCGGCTGCGAGACCAACACTTCTTGGGGCTGGGCAg 239834
Qy      41 AaMlyAaRProProTyLeuGlyGlnIleGlyAaGSerIyaAaG 55
Db      239835 AGCAAGCGGCTCCCAAGCTGGGCGAGATCGGCGGAGCAAGGCG 239879

RESULT 14
LOCUS      AC109006      259224 bp      DNA      linear      HTG 26-SEP-2002
DEFINITION      Rattus norvegicus clone CH230-44119, *** SEQUENCING IN PROGRESS
ACCESSION      AC109006
VERSION      AC109006.5      GI:2321630
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.

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SOURCE ORGANISM

Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE AUTHORS

1 (bases 1 to 259224)
Munz, D., Marle, Metzger, M., Lee, A., Adams, S., Adams, C., Alder, J., Allen, C., Allen, H., Albrooks, S., Amin, A., Angiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benhmed, F., Biewald, K., Blair, J., Blankensbury, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabisi, A., Gant, R., Garcia, A., Garner, T., Garza, M., Gebrgeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hui, S., Hume, J., Idubird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovac, C., Kovacs, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshaw, L., Loulsegue, H., Lozano, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E., Maubrey, S., McLeod, M. P., McNeill, T. Z., Meenen, J., Milosavljevic, A., Miner, G., Minja, R., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munida, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokileh, O., Okunuga, G., Olampunsegon, A., Pal, S., Parks, K., Patel, N., Paul, H., Perez, A., Perez, L., Fiankhoch, C., Pieper, F., Polinder, A., Popovic, D., Primus, B., Pu, L., L., Puzo, M., Quirio, J., Rachlin, E., Reeves, K., Reiser, M. A., Reish, R., Kelly, B., Kelly, M., Ken, I., Kenter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Saverly, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartbeyn, A., Sisson, I., Sitter, C. D., Smag, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejo, Z., Usmani, K., Valas, R., Vera, V., Villamas, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., Wiley, F., Williams, G., Willson, R., Wleciyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, S., Zhao, S., Dunn, D., von Weidenhausen, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G., and Gibbs, R. A.

sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GPPS
Center clone name: CH230-44119
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 162075 bases at least Q40
Consensus quality: 169729 bases at least Q30
Consensus quality: 175172 bases at least Q20
Estimated insert size: 196813; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 19653: contig of 19653 bp in length
* 19654 19753: gap of unknown length
* 19754 103202: contig of 83449 bp in length
* 103203 103303: gap of unknown length
* 103304 151034: contig of 47732 bp in length
* 151035 151134: gap of unknown length
* 151135 173513: contig of 22379 bp in length
* 173514 173613: gap of unknown length
* 173614 228828: contig of 55215 bp in length
* 228829 228928: gap of unknown length
* 228929 245283: contig of 16355 bp in length
* 245284 245384: gap of unknown length
* 245385 246664: contig of 1281 bp in length
* 246665 246782: gap of unknown length
* 246783 247882: contig of 1018 bp in length
* 247883 249267: gap of unknown length
* 249268 249367: gap of 185 bp in length
* 249368 251556: contig of 2189 bp in length
* 251557 251657: gap of unknown length
* 251658 253199: contig of 1543 bp in length
* 253200 253300: gap of unknown length
* 253301 254502: contig of 1203 bp in length
* 254503 254603: gap of unknown length
* 254604 259224: contig of 4622 bp in length.

FEATURES

source

1. .259224

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-44119"

1. .1160

/note="wgs contig"

18526. .19653

/note="wgs contig"

19654. .19753

/estimated length=unknown

33930. .35449

/note="wgs contig"

103203. .103302

/estimated length=unknown

119013. .122247

/note="wgs contig"

FEATURES

source

1. .259224

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-44119"

1. .1160

/note="wgs contig"

18526. .19653

/note="wgs contig"

19654. .19753

/estimated length=unknown

33930. .35449

/note="wgs contig"

103203. .103302

/estimated length=unknown

119013. .122247

/note="wgs contig"


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Db      258  ATGTCGAGGTCCTGCTGACCGAGAGGAGAAATGACCGATACCGAGCCGACACTGAT 317
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Search completed: March 9, 2006, 00:28:53
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RESULT 2
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AL391357 20 GI:16501137
VERSION AL391357
KEYWORDS HIG; CaMKII α lpha; CDA; cytidine deaminase; DOST; FLJ00387;

SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 195076)
Kimberley, A.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (13-May-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
JOURNAL Clone requests: clonerequests@sanger.ac.uk
COMMENT
On Oct 26, 2001 this sequence version replaced gi:16304938.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep. This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chrl>
Rpl1-401M16 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pBAC3.6
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: vegas@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
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QY	601	TTCTTCGCGCGCGGAGCAAGCGCGCGCAACTGAGGAGATCGCGCGGAGCAAG	660
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REFERENCE 1
AUTHORS   Plumb, B
TITLES    Direct Substitution
JOURNAL   Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
          CB10 1SN, UK. E-mail enquiries: humquery@sanger.ac.uk
          Requester: clonerequest@sanger.ac.uk
          On Nov 10, 2000 this sequence version replaced gi:9797484.
COMMENT   ----- Genome Center
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          Center code: SC
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          Contact: humquery@sanger.ac.uk
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Chemistry: Dye-terminator Big Dye; 100% of reads
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Insert size: 147762; 1.2% error; agarose-fp
Quality coverage: 3.57x in Q20 bases; sum-of-contigs Quality
coverage: 3.10x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 16202 19430: contig of 3229 bp in length
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LOCUS Homo sapiens chromosome 1 clone RP11-419, WORKING DRAFT SEQUENCE,
DEFINITION 31 unordered pieces.
AC025224
AC025224.3 GI:7596970
HTG: HTGS PHASE1; HTGS_DRAFT.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 163801)
Waterston R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 163801)
Waterston R.H.
Direct Submission
Submitted (07-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63106, USA
On Apr 19, 2000 this sequence version replaced gi:7321912.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center Project name: H.NH0004L09
----- Summary Statistics -----
Sequencing vector: M13, 100%
Sequencing vector: plasmid, 0%

Chemistry: Dye-terminator ET; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 145820 bases at least Q40
Consensus quality: 150999 bases at least Q30
Consensus quality: 153311 bases at least Q20
Insert size: 185000; agarose-fp
Insert size: 160801; sum-of-contigs
Quality coverage: 3.57 in Q20 bases; agarose-fp
Quality coverage: 4.25 in Q20 bases; sum-of-contigs
----- NOTE: This is a 'working draft' sequence. It currently
* consists of 31 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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1641 1740: gap of unknown length
1741 3443: contig of 1703 bp in length
3444 3543: gap of unknown length
3544 4790: contig of 1247 bp in length
4791 4890: gap of unknown length
4891 6777: contig of 1887 bp in length
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6879 8114: contig of 1237 bp in length
8115 8215: gap of unknown length
8216 9912: contig of 1698 bp in length
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58815 58914: gap of unknown length
58916 63420: contig of 4506 bp in length
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DEFINITION	MOLECULES EXPRESSED IN HIPPOCAMPUS.				
ACCESSION	BD276315				
VERSION	BD276315.1	GI:33086083			
KEYWORDS	JP 2002543833-A/1.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Homidae; Homo.				
REFERENCE	1 (bases 1 to 1581)				
AUTHORS	Baughn, M. R., Lal, P., Yue, H., Tang, T. Y., Azimzai, Y. and Kaser, M. R.				
TITLE	MOLECULES EXPRESSED IN HIPPOCAMPUS				
JOURNAL	Patent: JP 2002543833-A 1 24-DEC-2002;				
	INCYTE GENOMICS INC, Matthew R KASER, Preeti LAL, Henry YUE, Tom Y				
	TANG, Mariah R BAUGHN, Yelda AZIMZAI				
COMMENT	OS Homo sapiens				
	PN JP 2002543833-A/1				
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	PF 10-MAY-2000 JP 2000618442				
	PI 17-MAY-1999 US 09/313300				
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DEFINITION	Sequence 1 from Patent WO0212279.		
ACCESSION	AX451459		
VERSION	AX451459.1 GI:21698460		
KEYWORDS	.		
SOURCE ORGANISM	Homo sapiens (human)		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1		
AUTHORS	Bihain,B., Bour,B. and Bougueleret,L.		
TITLE	Schizophrenia related gene and protein		
JOURNAL	Patent: WO 0212279-A 1 14-FEB-2002;		
GENSET (PR)			
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Oy	2158	GTTGTTATGAGATGATGATTGATGACGTGCGAATAATATGACCGAACAGCACCT	2217
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Db	312	-CTGCTGTCTACT -CCCCAAAGCAATGATTAAGGAGAGAAATAGAACGCGGTAAc	369
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Db	429	CCACAGTAAGTAATCAACAACCTGTATCTGTAT -ATGCCCGAGACAGATTAAGCGCA -AGG	486
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Db	487	AGGAGAGAGAGAGAGAGAGAGCTTGCGC -CCTTACAAATTAATAATAAAAAAAAAAT	545
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Db	546	TAATAATATTAATCCCTATA-----TCCCATATTAAGATATTAAGAATC	589
Qy	2518	TCAGTGTGACACTATTTTGGCAAAATTAATATCATCTTTCTTTTATATAGGGTGAATATGCG	2577
Db	590	TCAGT-----GCATATATGGCAAAATTAATATCCATTTCTTTTATATACGG-----ATATTT	641
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DEFINITION	Homo sapiens calcium/calmodulin-dependent protein kinase II		
ACCESSION	AY204901	mRNA, complete cds.	
VERSION	AY204901.1	GI:30959105	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	Li, N. and Cao, X.		
AUTHORS	Direct Submission		
TITLE	Submitted (19-DEC-2002) Institute of Immunology, Second Military		
JOURNAL	Journal		
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QY 99 CCGGCGGCGGCTCCCGGAGTGGCGCTCTCTGAGTCCGCGGCTTCGCGAGGAGGAGC 158
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QY 219 CCGAGAGATGTAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 278
Db 121 CCGAGAGATGTAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180

QY 279 AGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 338
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QY 339 GCGGCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 398
Db 241 GCGGCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300

QY 399 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 458
Db 301 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360

QY 459 GGTGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 518
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DEFINITION NRI-AB5C.
ACCESSION AJ324422
VERSION AJ324422.1 GI:15868801
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
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Kutsenko, A.S., Glatkuljin, R.Z., Al-Amin, A.N., Wang, F., Kvashina, S.M.,
Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V.,
Levitky, V.G., Kojichanov, N.A., Protopopov, A.I., Kashuba, V.I.,
Kiselev, L.L., Maeser, W., Wahlestedt, C. and Zabarovsky, E.R.
Noci flanking sequences: a tool for gene discovery and verification
of the human genome
JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)
PUBMED 12136098
REFERENCE 2 (bases 1 to 616)
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AUTHORS Zabarovsky, E.R.
TITLE Direct Submission
JOURNAL Microbiology and Tumorigenesis Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden

FEATURES

source

Location/Qualifiers
1. 616
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ORIGIN

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Best Local Similarity 94.3%; Pred. No. 3.5e-59;
Matches 581; Conservative 0; Mismatches 32; Indels 3; Gaps 2;

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QY 77 CCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 135
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QY 136 CCGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 195
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QY 196 CCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 255
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QY 256 CAGGCACTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 315
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QY 316 GCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 375
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QY 556 GACGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 615
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QY 616 CAGAGCAAGGCGGCGG 631
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PF	09-SEP-2004; 2004US-00936773.
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PR	30-JUL-1997; 97US-0054211P.
PR	30-JUL-1997; 97US-0054212P.
PR	30-JUL-1997; 97US-0054213P.
PR	30-JUL-1997; 97US-0054214P.
PR	30-JUL-1997; 97US-0054215P.
PR	30-JUL-1997; 97US-0054217P.
PR	30-JUL-1997; 97US-0054218P.
PR	30-JUL-1997; 97US-0054234P.
PR	30-JUL-1997; 97US-0054236P.
PR	18-AUG-1997; 97US-0055668P.
PR	18-AUG-1997; 97US-0055669P.
PR	18-AUG-1997; 97US-0055972P.
PR	18-AUG-1997; 97US-0056534P.
PR	18-AUG-1997; 97US-0056543P.
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PR	18-AUG-1997; 97US-0056561P.
PR	19-AUG-1997; 97US-0056727P.
PR	19-AUG-1997; 97US-0056730P.
PR	29-JUL-1998; 98WO-US612549.
PR	26-JAN-1999; 99US-00236557.
PR	21-SEP-2000; 2000US-00665684.
PR	30-MAR-2001; 2001US-00820649.
PR	05-JUN-2001; 2001US-0295558P.
PR	04-JUN-2002; 2002US-00160162.
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PA	(HUMA-) HUMAN GENOME SCT INC.
XX	
PB	Ruben SM, Feng P, Lafleur DM, Moore PA, Shi Y, Kyaw H, Li Y,
PI	Zeng Z, Carter KC, Endress GA, Wei Y, Fan P, Rosen CA;
PT	WPI; 2005-161941/17.
XX	
DR	P-PSDB; ADY25460.
XX	
PT	New nucleic acid molecule encoding human secreted protein, useful for preventing, treating, or ameliorating immune system, blood, inflammatory, infectious, cardiovascular, respiratory, neurological, endocrine, or reproductive disorders.
XX	
PS	Claim 1; SEQ ID NO 25; 309pp; English.
XX	
CC	The invention comprises the amino acid and coding sequences of novel human secreted proteins and peptides. The DNA and protein sequences of the invention are useful for treating or ameliorating cancer, arthritis, CC ashma, AIDS, rheumatoid arthritis, inflammatory bowel disease, sepsis, CC acne, psoriasis, atherosclerosis, stroke, thrombosis, wound healing, CC Alzheimer's Disease, Parkinson's Disease, autism, obsessive compulsive disorder, graft-versus-host diseases, immune system disorders, blood CC disorders, inflammatory conditions, infectious diseases, CC hyperproliferative disorders, renal disorders, cardiovascular disorders, CC respiratory disorders, neurological disorders, endocrine disorders, or CC reproductive disorders. The present sequence is that of a cDNA which encodes a novel human secreted protein of the invention.
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XX	
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QY	2278	AGTTATTGGCAAAAAGCAAGAAAAGAGAGCACTTGAATTTAATTACTACTGCTGAC	2337
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QY	2398	AGAGGAGAGGAGAGGAGAGAGGCTGTGGCTCTCTGCAAAAATTTAAAATTTAA	2457
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QY	2518	TGAGTTCAGACTATTGTCAAAATTAATATGCAATTCCTTTTATATAGCGTAAATG	2577
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QY	2578	GCAATTAATAGATCGATTTTGAAACAATTATAGAGGAGACACAGGTGTTTGA	2637
Db	532	GCAATTAATAGATCGATTTTGAAACAATTATAGAGGAGACACAGGTGTTTGA	591
QY	2638	TGTTCGCAATCTTCGCTGATTTGGCTGTCCCAATGTTTACATTTATTAATCTG	2697
Db	592	TGTTCGCAATCTTCGCTGATTTGGCTGTCCCAATGTTTACATTTATTAATCTG	651
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QY	2758	CTTGAGATGTCACAAAATTAATGAAATATGATCTCTGTATATCTGTGTTATTTG	2817
Db	712	CTTGAGATGTCACAAAATTAATGAAATATGATCTCTGTATATCTGTGTTATTTG	771
QY	2818	TCTTTAGAGAGTTATCAGAAATGTGTGTTTAAACAAGAGAGAACTTTCTATGA	2877
Db	772	TCTTTAGAGAGTTATCAGAAATGTGTGTTTAAACAAGAGAGAACTTTCTATGA	831
QY	2878	CATAGAAAAGATTTTATTTTAAATGATGTGTTAAAGCTGTGTTCTTGATGCTG	2937
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Db	892	CTATCTGCGCCAGTTATATGCAATATGACACATTTTATATGTCAAAA-----	951
QY	2992	ACACACACACACACACACACACACACACAGAAAACAAAGAAAATTTGTTGACTT	3051
Db	952	ACACACACACACACACACACACACACACAGAAAACAAAGAAAATTTGTTGACTT	1011
QY	3052	TTCCTACTCTCCCTGCACTGTGTGTGTGAGACCTGTTTATTTCTATATATATG	3111
Db	1012	TTCCTACTCTCCCTGCACTGTGTGTGTGAGACCTGTTTATTTCTATATATATG	1071
QY	3112	CAGTTATATCTCTTTATATGACTGTATGAAAAATTTGATATCAAGATGCAAT-TC	3170
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ID AD024238 standard; DNA; 2058 BP.			
XX			

AC	ADQ24238;
DT	26-AUG-2004 (first entry)
XX	
DE	Human soft tissue sarcoma-upregulated DNA - SEQ ID 7056.
XX	
KM	soft tissue sarcoma; cytoelastic; gene therapy; vaccine; screening; human;
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XX	
XX	Homo sapiens.
XX	
PN	N02004048938-A2.
PD	
XX	10-JUN-2004.
XX	
PF	26-NOV-2003; 2003WO-US038193.
PR	
XX	26-NOV-2002; 2002US-0429739P.
PA	(PROT-) PROTEIN DESIGN LABS INC.
PI	Aziz N, Ginsburg NM, Zlotnick A;
DR	WPI; 2004-441208/41.
XX	
PT	Early detection of soft tissue sarcoma comprises determining expression
PT	of a gene in a first soft tissue sample and a normal soft tissue sample
PT	and comparing the gene expression, also useful in treating soft tissue
PT	sarcoma.
XX	
PS	Example 2; SEQ ID NO 7058; 210pp; English.
CC	The invention relates to a novel method for detecting soft tissue sarcoma
CC	which comprises obtaining a first soft tissue sample from an individual
CC	and a normal soft tissue sample from the same or different individual,
CC	determining the expression of a gene in both samples and comparing the
CC	expression of the gene in both soft tissue samples, where a higher level
CC	of protein expression in the first soft tissue sample indicates the
CC	presence of soft tissue sarcoma. The method of the invention has
CC	cytostatic applications and may be useful for detecting soft tissue
CC	sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC	acid sequences may be useful in diagnostic and screening applications.
CC	The current sequence is that of a human soft tissue sarcoma-upregulated
CC	DNA of the invention. The current sequence is not shown within the
CC	specification per se but was submitted in CD format by the inventor.
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Query Match	31.4%; Score 1002.4; DB 12; Length 2058;
Best Local Similarity	99.2%; Pred. NO. 5.6e-167;
Matches 1030; Conservative	0; Mismatches 1; Indels 7; Gaps 2
OY	2158 GTTGTTATTGAAAGTAGATGATGATGACGTGCTGAATAAATATGACCGACAAGCAACT 221
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OY	2278 AGTTATTGGCAAAAAGATGAAAGAAAGAAABCACTTTGAAATTTTATCTAGCTTGTCAC 233
Db	1678 AGTTATTGGCAAAAAGATGAAAGAAAGAAABCACTTTGAAATTTTATCTAGCTTGTCAC 1611
OY	2338 CCAAGATGAATTCACAAACCTGTAATCTGGTATCAGGCCGAGACACATGATGGGGAGAGG 239
Db	1618 CCAAGATGAATTCACAAACCTGTAATCTGGTATCAGGCCGAGACACATGATGGGGAGAGG 1555
OY	2398 AAGAGAGAGAGAGAGAGAGAGGCTCTGGGGCTCTCTGCAGAAAAATTAATAAATAAATAA 245
Db	1558 AAGAGAGAGAGAGAGAGAGAGGCTCTGGGGCTCTCTGCAGAAAAATTAATAAATAAATAA 1499
OY	2458 TAATAATTTTAAAAATTAATAAATTCAGTATATACATATTAAGAAAAATTAATAAAGAGTC 251

Db	1498	TAAATTTTAAAAATTAATAAAAATTCACATATATACATATAAAGAAATTAAGAAAGTC	1439
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Qy	3171	AAATGCCAAAGAGCTTTT	3188
Db	778	AAATGCCAAAGAGCAATT	761
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DT	20-MAY-2004	(first entry)	
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DE	Marker gene SEQ ID NO:450.		
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XX	bronchial asthma; chronic obstructive pulmonary disease;		
KW	respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;		
KW	gene therapy; marker gene; gene; ds.		
OS	Homo sapiens.		
XX			
XX	EP1394274-A2.		
FN			
PD	03-MAR-2004.		
XX			
XX	04-AUG-2003; 2003EP-00254857.		
XX			
XX			

[illegible]

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Qy	2938	CTATCGCCCAAGTTAAAGCAATGACATTTTAAATGACAAAA-----ACACAC	2991
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Qy	2992	AC	3051
Db	449	AC	390
Qy	3052	TTCTAACCTCCCTGACAGTCTGTGTGTGAGACACCTGTTATTTCTCAATATATGT	3111
Db	389	TTCTAACCTCCCTGACAGTCTGTGTGTGAGACACCTGTTATTTCTCAATATATATGT	330
Qy	3112	CAGTTATTTCTTTTAAATGACCTGTAAAAAAATGTATACACAGTGCACAAAT--TCTTG	3170
Db	329	CAGTTATTTCTTTTAAATGACCTGTAAAAAAATGTATACACAGTGCACAAATATCTTG	270
Qy	3171	AAATGCCAAAGGCACTTT 3188	
Db	269	AAATGCCAAAGGCACTTT 252	
RESULT 10			
ID	ADR25935		
XX	ADR25935 standard; DNM; 1321 BP.		
AC	ADR25935;		
DT	21-OCT-2004 (first entry)		
XX	Breast cancer prognosis marker #1796.		
DS			
XX	de; breast cancer; prognosis; gene expression; diagnosis.		
KM			
XX	Homo sapiens.		
OS			
XX	WO2004065545-A2.		
XX			
PD	05-AUG-2004.		
XX			
PF	15-JAN-2004; 2004MO-US001100.		
XX			
PR	15-JAN-2003; 2003US-00342887.		
XX			
PA	(ROSE-) ROSETTA INPHARMATICS LLC.		
PA	(NECA-) NETHERLANDS CANCER INST.		
XX			
PI	Van't Veer LJ, He Y;		
XX			
DR	WPI; 2004-593473/57.		
XX			
PT	Classifying a breast cancer patient according to prognosis comprises		
PT	determining the similarity between the level of expression of each of		
PT	five genes in a cell sample taken from patient; to control levels.		
PS	Disclosure: SEQ ID NO 1796; 226bp; English.		
XX			
CC	The invention relates to a method of classifying a breast cancer patient		
CC	according to prognosis by determining the similarity between the level of		
CC	expression of each of five genes for which markers are listed in the		
CC	specification, in a cell sample taken from the breast cancer patient, to		
CC	control levels of expression for each respective five genes to obtain a		
CC	patient similarity value. The methods are useful for classifying a breast		
CC	cancer patient according to prognosis. Kits and computer program products		
CC	are useful for data analysis using the diagnostic, prognostic and		
CC	statistical methods of the invention. This sequence corresponds to a		
CC	marker used in the method of the invention.		

Db 700 CCACGATGAAATCAACACCTGATCTGTATTCAGCCGGGAGACAGATGAGCGGAGAG 759
 Qy 2398 AG 2456
 Db 760 AG 819
 Qy 2457 ATAAAT 2516
 Db 820 ATAAAT 879
 Qy 2517 CTGAGTTCAGCTATTTGTCATTAATATATATATATATATATATATATATATATATAT 2576
 Db 880 CTGAGTTCAGCTATTTGTCATTAATATATATATATATATATATATATATATATATAT 939
 Qy 2577 CCAGATTTAT 2636
 Db 940 CCAGATTTAT 999
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 Db 1000 GTGTGGATTTCTGCGATGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1059
 Qy 2697 AATGCTTCGTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2756
 Db 1060 AATGCTTCGTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1119
 Qy 2757 CCTTGGATTTGCAAAAATTCAGAAAATGATCTGTGATATCTGCTTATTTTGTCTC 2816
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 Db 1180 ATCTTGAAGTTATTCAGATATGCTTTTAAACAAAGAGAACTTTTCTAAGGATGAT 1239
 Qy 2877 ACATGAAAGATTTATTTTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 2936
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 Db 1300 GCTATCTGCCAGATTAATGCAATGAGACATTTTATGTCAGAAAACACACACACAC 1359
 Qy 2997 -----CAC 3049
 Db 1360 NNN 1419
 Qy 3050 TTTTCTACTCTCCCTTGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3109
 Db 1420 TTTTCTACTCTCCCTTGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1479
 Qy 3110 GTCACTTATCTCTTATATGAGCTGTAAATAATGTAATCAAGATGCAAT-TCT 3168
 Db 1480 GTCACTTATCTCTTATATGAGCTGTAAATAATGTAATCAAGATGCAATATCT 1539
 Qy 3169 TGAATGCAAAAGGCTTTT 3188
 Db 1540 TGAATGCAAAAGGCAATT 1559
 RESULT 14
 AB060975
 ID AB060975 standard; cDNA; 873 BP.
 XX AC AB060975;
 XX DT 26-FEB-2003 (first entry)
 XX DE PRO1489 protein encoding sequence.
 XX KW Neuroprotective; immunomodulator; cancer; chromosome 1; cytosolic;
 XX anti-inflammatory; gene therapy; nutritional supplement; wound; burn;
 KW ulcer; Alzheimer's disease; Huntington's disease;
 KW amyotrophic lateral sclerosis; autoimmune disorder; inflammation;

KW vulnerable; gene; ss.
 XX OS Homo sapiens.
 XX PN WO200231111-A2.
 XX PD 18-APR-2002.
 XX PF 11-OCT-2001; 2001WO-US027760.
 XX PR 12-OCT-2000; 2000US-00687527.
 XX PA (HYSB-) HYSBQ INC.
 XX PI Tang YF, Liu C, Zhou P, Asundi V, Zhang J, Zhao QH, Ren F;
 XX PI Xue AJ, Yang Y, Wehrman T, Dermanac RT;
 XX DR N-Psdb; ABP43731.
 XX DR WPI; 2002-426278/45.
 XX PT New polypeptides and their encoded proteins, useful as nutritional
 XX PT sources or supplements, or in gene therapy, particularly for treating
 XX PT wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
 XX PT inflammation.
 XX PS Claim 1; SEQ ID # 188; 357bp + Sequence Listing; English.
 XX CC The invention relates to 446 newly isolated polynucleotide sequences. The
 XX CC activity of polynucleotides of the invention may be described as,
 XX CC vulnerability, neuroprotective, immunomodulator, cytosolic and anti-
 XX CC inflammatory. Compositions comprising nucleic acids of the invention are
 XX CC useful for treating a mammalian subject, or as nutritional sources or
 XX CC supplements. These are useful in gene therapy, particularly for treating
 XX CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
 XX CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or
 XX CC inflammation. The nucleic acids and polypeptides are also useful in
 XX CC diagnostic and research methods. The sequences given in records AB060788-
 XX CC AB061233 represent polynucleotides of the invention. NOTE: The sequence
 XX CC data for this patent did not form part of the printed specification, but
 XX CC was obtained in electronic format directly from WIPO at
 XX CC ftp://wipo.int/pub/published_pct_sequences
 XX CC
 XX CC Sequence 873 BP; 304 A; 144 C; 174 G; 251 T; 0 U; 0 Other;
 SQ
 Query Match 24.8%; Score 791.4; DB 6; Length 873;
 Best Local Similarity 99.6%; Pred. No. 7.1e-130;
 Matches 814; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
 Qy 2205 CGACAGGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2264
 Db 53 CGACAGGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 112
 Qy 2265 GAACGGCGGTAACTGTTATGCAAAAGCATGAAAGAGAAAGCACTTGAATTTAT 2324
 Db 113 GAACGGCGGTAACTGTTATGCAAAAGCATGAAAGAGAAAGCACTTGAATTTAT 172
 Qy 2325 ACTAGCTTCTACCCAGATGAATCAACACCTGTATCTGTATCGAGCGGGAGACAG 2384
 Db 173 ACTAGCTTCTACCCAGATGAATCAACACCTGTATCTGTATCGAGCGGGAGACAG 232
 Qy 2385 ATGAGCGAG 2444
 Db 233 ATGAGCGAG 292
 Qy 2445 ATAAAT 2504
 Db 293 ATAAAT 352
 Qy 2505 ATAAAT 2564
 Db 353 ATAAAT 412
 Qy 2565 CGGTGAATTTGCGCAATTAATATGATGATTTGCAACCACTTAATGAAGCGGCAACAC 2624


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Db 1038 CGCATTATATGATCTGGA-TTTGAACACTTAATGAAAGCGGCAACACAGGTGTTTGAG 1096
QY 2637 GTGTTGGCATTCCTCGTATATTTGGCTGTCCGAATGTTACATATTTATCTTGCAAA 2696
Db 1097 GTGGTGGCATTCCTCGTATATTTGGCTGTCCGAATGTTACATATTTATCTTGCAAA 1156
QY 2697 AATGGTCTGTGCACTTGGATGTAAATGCTGTCAGTTTATTTTGTGTTA 2755
Db 1157 AATGGTCTGTGCACTTGGATGTAAATGCTGTCAGTTTATTTTGTGTTA 1216
QY 2756 T----CCTTGGATGTACAAAAATTCAGAAAAATGATCTGTAGATATTCGTTTATTT 2811
Db 1217 TTATCTGTGTGATGTACAAAAATTCAGAAAAATGATCTGTAGATATTCGTTTATTTA 1275
QY 2812 TGGTCATCTTTAGAGTTATCAGAGATGTGTTTAAACAAGAAGAACTTTCTAAGGA 2871
Db 1276 GGGTCATCTTTAGAGTTATCAGAGATGTGTTTAAACAAGAAGAACTTTCTAAGGA 1335
QY 2872 ATGATACATAGAAAAAGATTTTATTTTAAATG--AGTTGTAAAGCTTGTTCTTGTTG 2930
Db 1336 ATGATACATAGAAAAAGATTTTATTTTAAATGAGTAAAGCTTGTTCTTGTTG 1395
QY 2931 CT-GCAAGCTATCTGCCCAAGTTAATGCAATGGAACA---TTTTTATGTGCAAAAAA 2986
Db 1396 CTGGCAAGCTATCTGCCCAAGTTAATGCAATGGAACAATTTTATGTGCAAAAAA 1455
QY 2987 CACACACACACACACACACACACACACACACACACACACACACACACACACACACAC 3033
Db 1456 CACACACACACACACACACACACACACACACACACACACACACACACACACACACAC 1502
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Title: US-10-071-645-3

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Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2.*
3: gb_est3.*
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5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_gse1.*
10: gb_gse2.*
11: gb_gse3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	1018.4	31.9	1566	4	CR604926 full-length
2	1009.8	31.4	1321	7	AR116637 Homo sapi
3	822.4	25.8	923	7	CN803331 ILLUMIGEN
4	795.4	24.9	976	7	CN802133 ILLUMIGEN
5	789.4	24.8	954	7	CN843673 ILLUMIGEN
6	787.4	24.7	953	7	CN803102 ILLUMIGEN
7	787.4	24.6	953	7	CN803224 ILLUMIGEN
8	785.6	24.6	954	7	CN845555 ILLUMIGEN
9	783.6	24.6	950	7	CN646790 ILLUMIGEN
10	783	24.6	952	7	CN646545 ILLUMIGEN
11	782.6	24.5	955	7	CN644007 ILLUMIGEN
12	780.8	24.5	954	7	CN646445 ILLUMIGEN
13	780.6	24.5	911	7	CN802110 ILLUMIGEN
14	779.4	24.4	951	7	CN647038 ILLUMIGEN
15	779.4	24.4	954	7	CN803392 ILLUMIGEN
16	777.4	24.4	1083	4	CR606015 full-length
17	776.4	24.3	964	7	CN646785 ILLUMIGEN
18	772	24.2	953	7	CN646019 ILLUMIGEN
19	766.4	24.0	955	7	CN805169 ILLUMIGEN
20	762.6	23.9	931	5	BK419572 ILLUMIGEN
21	757.2	23.7	955	7	CN802272 ILLUMIGEN
22	756.6	23.7	1020	7	CN803473 ILLUMIGEN

23	752.6	23.6	951	7	CN802081 ILLUMIGEN
24	749.8	23.5	944	7	CN803534 ILLUMIGEN
25	746.8	23.4	955	7	CN801954 ILLUMIGEN
26	745	23.4	1001	7	CN802311 ILLUMIGEN
27	735.2	23.1	808	5	BU570962 AGENCOURT
28	728.2	22.8	747	3	BQ018543 UI-H-DH1-
29	728	22.8	1026	7	CN643857 ILLUMIGEN
30	727.4	22.8	890	7	CN645235 ILLUMIGEN
31	726.6	22.8	806	7	CN642220 ILLUMIGEN
32	721.4	22.6	956	7	CN805265 ILLUMIGEN
33	721	22.6	967	7	CN641685 ILLUMIGEN
34	720	22.6	993	7	CN802904 ILLUMIGEN
35	711.4	22.3	968	7	CN805606 ILLUMIGEN
36	705.2	22.1	967	7	CN644185 ILLUMIGEN
37	704.6	22.1	997	7	CN803212 ILLUMIGEN
38	704.2	22.1	853	5	BU928986 AGENCOURT
39	699.8	21.9	914	7	CO645211 ILLUMIGEN
40	688.8	21.6	1004	7	CN801895 ILLUMIGEN
41	685.2	21.5	992	7	CN802324 ILLUMIGEN
42	683	21.4	656	7	CN428017 ILLUMIGEN
43	677.2	21.2	953	7	CO645289 ILLUMIGEN
44	656.8	20.6	661	3	BQ000750 UI-H-DH1-
45	656.8	20.6	990	7	CN803111 ILLUMIGEN

ALIGNMENTS

RESULT 1
LOCUS CR604926 1566 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DF038YH05 of Fetal brain of Homo sapiens (human).
ACCESSION CR604926
VERSION CR604926.1 GI:50485733
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1566)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invtrogen.com/ invtrogen Corporation 1600 Paradies Avenue
2 (bases 1 to 1566)
REFERENCE Genoscope
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BE191 91006 Every cedex - FRANCES (E-mail: seque@genoscope.cns.fr - Web: www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES
location/Qualifiers
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF038YH05"
/tissue_type="Fetal brain"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 31.9%; Score 1018.4; DB 4; Length 1566;
Best Local Similarity 99.8%; Pred. No. 1.9e-193;
Matches 1030; Conservative 0; Mismatches 1; Indels 1; Gaps 1;


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Db      929 TCAATGACGATTTGTCAGAAATTAATTCATTTCTTTTATATACCGGTAATATTC 870
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Db      869 GCAATTAATGATCTGCAATTTTGAACCACTTAATAGACGGCAACACAGGTTTGAAG 810
Qy      2638 TGTGGCAATCTTGTGCTGATTTGGCTGTGTCGCAATGTTTACATTTTAACTTGGCAAA 2697
Db      809 TGTGGCAATCTTGTGCTGATTTGGCTGTGTCGCAATGTTTACATTTTAACTTGGCAAA 750
Qy      2698 ATGTTCTGTGCACTGAGATGTAATGCTGTCAGTTTATTTTATTTTATGTTATTC 2757
Db      749 ATGTTCTGTGCACTGAGATGTAATGCTGTCAGTTTATTTTATTTTATGTTATTC 690
Qy      2758 CTGGATGTAACAAAATTAATCAGAAAATGATCTCTGTAGATTTCTGTTTATTTGGTCA 2817
Db      689 CTGGATGTAACAAAATTAATCAGAAAATGATCTCTGTAGATTTCTGTTTATTTGGTCA 630
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Qy      2878 CATGAAAAGATTTTATTTTAAATGATGTAAGCTGTGTTCTTGTGTCGAG 2937
Db      569 CATGAAAAGATTTTATTTTAAATGATGTAAGCTGTGTTCTTGTGTCGAG 510
Qy      2938 CATGTCGCCAATTAATGCAATGCAACATTTTATGTCAGAAA-----ACACAC 2991
Db      509 CATGTCGCCAATTAATGCAATGCAACATTTTATGTCAGAAAACACACACAC 450
Qy      2992 ACACACACACACACACACACACACACACACACACACACACACACACACACAC 3051
Db      449 ACACACACACACACACACACACACACACACACACACACACACACACACACAC 390
Qy      3052 TTTCACTTCCCTTCAGCTGTGTTGTGAGACGCTGTTTATTTCTTAAATTAAT 3111
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Qy      3112 CAGTTTATCTCTTAAATGACTGTAAATAATGTAATCAAGAATGCCAAAT-TCCTG 3170
Db      329 CAGTTTATCTCTTAAATGACTGTAAATAATGTAATCAAGAATGCCAAATTCCTG 270
Qy      3171 AATGCCAAAAGGCTTT 3188
Db      269 AATGCCAAAAGGCAATTT 252

RESULT 3
CN803331      983 bp      mRNA      linear      EST 26-MAY-2004
LOCUS      ILLUMIGEN MCO 32763 Katze MM8R Macaca mulatta cDNA clone
DEFINITION      IBTUM-11357 5' similar to Bases 1 to 983 highly similar to human
                Cakutinalpha (hs.197922), mRNA sequence.
ACCESSION      CN803331
VERSION      CN803331.1 GI:47699307
KEYWORDS      EST
SOURCE      Macaca mulatta (rhesus monkey)
ORGANISM      Macaca mulatta
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Cercopithecoidea; Cercopithecinae; Macaca.
REFERENCE      1 (bases 1 to 983)
                Magness, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B.,
                Prohl, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
                Iadonato, S.P.
                Analysis of the Macaca mulatta transcriptome and the sequence
                divergence between Macaca and human
                Genome Biol. 6 (7), R60 (2005)
TITLE      JOURNAL
                PUBMED
                CONTACT: C. Magness
                Illumina Biosciences Inc.
                2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
                Tel: 2063780400

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FEATURES
Source      1..983
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              /mol_type="mRNA"
              /strain="indian"
              /db_xref="taxon:9544"
              /clone="IBIDW:13297"
              /sex="female"
              /dev_stage="adult"
              /lab_host="R. coli: SOLR"
              /note="Organ: brain; Vector: Uni-ZAP XR; Site 1: Ecor I;
              Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
              kit (catalog #200400) and ZAP-cDNA GigaPack III Gold
              Cloning Kit (catalog #200450)"

ORIGIN
Query Match      25.8%; Score 822.4; DB 7; Length 983;
Beet Local Similarity 95.2%; Pred. No. 3.9e-154;
Matches 906; Conservative 0; Mismatches 31; Indels 15; Gaps 5;

Qy      2249 TTAAGGAGAGAAATTAAGACCGCGGTAACAGTTATTGGCAAAAAGCATGAAAGAAAG 2308
Db      8 TAAAGAGAGAAATTAAGACCGCGGTAACAGTTACTGGCAAAAAGCATGAAAGAAAG 67
Qy      2309 CACTTGAATTTTATTAATCTAGCTTGCTACCAAGATGAATTAACAACCTGATCTGGTA 2368
Db      68 CACTTGAATTTTATTAATCTAGCTTGCTACCAAGATGAATTAACAACCTGATCTGGTA 127
Qy      2369 TCAGGCGGAGACAGATGAGTGAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2428
Db      128 TCAGGCGGAGACAGATGAGTGAGGCG--TGAAGAGAGAGAGAGAGAGAGAGAGAGAG 184
Qy      2429 CTCTGCAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 2488
Db      185 CTCTGCAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 244
Qy      2489 AT--ACACATTAAGAAATTAATAATAATAATAATAATAATAATAATAATAATAATA 2546
Db      245 ATACACACATTAAGAAATTAATAATAATAATAATAATAATAATAATAATAATAATA 304
Qy      2547 TCGATTTCTTTTATTAACGGTGCAATTTGGCAATTAATGATCTGGAATTTGAACACT 2606
Db      305 TCGATTTCTTTTATTAACGGTGCAATTTGGCAATTAATGATCTGGAATTTGAACACT 364
Qy      2607 TAATGAGCGGCAACACAGGTGTTTGAAGTGGCAATTTCTGCTGATTTGGCTGTT 2666
Db      365 TAATGAGCGGCAACACAGGTATTTTGAAGTGGCAATTTCTGCTGATTTGGCTGTT 424
Qy      2667 CCCAATGTTTACATTAATTAATCTTGAACAAAATGTTCTGTGCACTTGGATGTAATGC 2726
Db      425 CCCAATGTTTACATTAATTAATCTTGAACAAAATGTTCTGTGCACTTGGATGTAATGC 484
Qy      2727 TGTCCAGTTTATTTTATTAATGTTGTTATCTTGGATGTAACAAAATTTCAAGAAATGA 2786
Db      485 TGTCCAGTTTATTTTATTAATGTTGTTATCTTGGATGTAACAAAATTTCAAGAAATGA 544
Qy      2787 TCTCTGTAGATTAATCTGTTTATTAATTTGGTCACTTTAGAGATTAACAGAAATGTTTAA 2846
Db      545 TCTCTGTAGATTAATCTGTTTATTAATTTGGTCACTTTAGAGATTAACAGAAATGTTTAA 604
Qy      2847 AACAGAGAGAACTTTTCTAGAGATGATACATAGAAAAG-----TTTTATTTTAA 2900

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[illegible][illegible]

[illegible]

REFERENCE	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
AUTHORS	Cercopithecidae; Cercopitheciinae; Macaca.
TITLE	1 (bases 1 to 954)
JOURNAL	Magnus C.L., Fellin P.C., Thomas M.J., Korth M.J., Agy M.B.,
PUBMED	Prohl S.C., Fitzgibbon M., Scherer C.A., Miner D.G., Katze M.G. and
COMMENT	Iadonato S.P. Analysts of the Macaca mulatta transcriptome and the sequence divergence between Macaca and human Genome Biol. 6 (7), R60 (2005) 15988449 Contact: C. Magnus illumigen Biosciences Inc. 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA Tel.: 2063780400 Fax: 2063780408 Email: cmagnus@illumigen.com Sequenced on 2004.03.10. 788 Q20 bases. PCR Primers FORWARD: CCTCCTAAGGAGGAACAAA BACKWARD: CACTATAGCGAAATGGTGA Insert Length: 954 Std Error: 0.00 Plate: CL000144 row: H column: 08 Seq primer: CCCTCACTAAGGAGAACAAA POLYA=Yes. Location/Qualifiers 1. 954 /organism="Macaca mulatta" /mol_type="mRNA" /strain="Indian" /db_xref="taxon:9544" /clone="IBIUM:8439" /sex="female" /dev_stage="adult" /lab_host="E. coli SOLR" /clone_lib="Katze_MMRB" /note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I; Site 2: Xho I; Created from strataene zap-cDNA synthesis kit [catalog #200400] and ZAP-CDNA GigaPack III Gold Cloning Kit [catalog #200450]" ORIGIN Query Match 24.6%; Score 785.6; DB 7; Length 954; Best Local Similarity 95.1%; Pred. 9.5e-147; Matches 846; Conservative 0; Mismatches 34; Indels 10; Gaps 3
Dy	2156 GTGTGTTTAATAAATATATGATTGATGAGCTGTCGTGAATAAATATGACCGACAAGCACT 2217
Dz	68 GTTGTTATTAATAATGATATGATGATTTGATGATGCTGTCTAATAAATATGACCGACAAGCACT 127
Ey	2218 CTGTGCTCTTAATCCGCCGAAGAAGCATATGATTAAGGAGAGATTAAGAACCGCGTAGC 2278
Fy	128 CTCGTGCTCTTAATCCGCCGAAGAAGCATATGATTAAGGAGAGATTAAGAACCGCGTAGC 187
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Jz	248 CCACGATGAATTAACAACTCTGATCTGATATCAGGCGCGGAGACAGATGAGCG--TG 304
Ky	2398 AGAAGAGAGAGAGAGAGAGCTCTGCGCTCTCTCTGCAAAAATTAATAAATAAATAA 2457
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My	2458 TAAATTTTAAATTAATAAATTAATTCATCTATAT -ACAATATTAAGAAATTAAGAAG 2515
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Oy	2516 TTCTAGTTGAGCTATTTGTCAAATTAATATCAATTTCTTTTATATACGATGATAT 2575
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QY 2576 GGGCAATTATGATCTGGAATTTTGAACCACTTAATGAGCGGCAACACAGGTGTTTGA 2635
DB 485 GGGCAATTATGATCTGGAATTTTGAACCACTTAATGAGCGGCAACACAGGTATTTGA 544
QY 2636 GGTGTGGCAATCTTCTGCTGATTTGCGTGTCCCAATGTTTACATTATTTATCTTGCA 2695
DB 545 GGTGTGGCAATCTTCTGCTGATTTGCGTGTCCCAATGTTTACATTATTTATCTTGCA 604
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QY 2931 CTGCAAGCTATCTGCCAGTTAATGCAATGCAACATTTTATGTCAGAAAACACA 2990
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RESULT 9
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DEFINITION 5' similar to Bases 1 to 360 highly similar to human CASK11alpha
(Hs197922), mRNA sequence.
VERSION CN646790
KEYWORDS CN646790.1 GI:47160233
SOURCE EST.
ORGANISM Macaca mulatta (rhesus monkey)
Macaca mulatta
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 950)
Magnee,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,
Prohl,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and
Iadonato,S.P.
TITLE Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human
JOURNAL Genome Biol. 6 (7), R60 (2005)
PUBMED 1598449
COMMENT Contact: C. Magnee
illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagnee@illumigen.com
Sequenced on 2004.03.11. 819 Q20 bases.
PCR primers
FORWARD: CCTCACTAAGGAGAACAAA
BACKWARD: CACTTAAGGCGAATGGCTA
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POLY=A=yes

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kit (catalog #200400) and ZAP-cDNA GigaPack III Gold
Cloning Kit (catalog #200450)"

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DB 128 CTTGGTGTAACTCCCAAGACATGATGATTAAGGAGAGATTAAGCGGCTAAC 187
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DB 248 CCACATGAAATCAACAACCTGATCTGATACAGCGGAGAGACAGATGAGGAGAG 304
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DB 305 AGAGAGAGAGAGAGAGAGAGCTGTGGCTCTCTGCAAAAATATTAATAATTA 364
QY 2458 TAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2515
DB 365 TAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 424
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QY 2576 GGGCAATTATGATCTGATTTTGAACCACTTAATGAGCGGCAACACAGGTGTTTGA 2635
DB 485 GGGCAATTATGATCTGATTTTGAACCACTTAATGAGCGGCAACACAGGTATTTGA 544
QY 2636 GGTGTGGCAATCTTCTGCTGATTTGCGTGTCCCAATGTTTACATTATTTATCTTGCA 2695
DB 545 GGTGTGGCAATCTTCTGCTGATTTGCGTGTCCCAATGTTTACATTATTTATCTTGCA 604
QY 2696 AAATGTTCTGTGCACTTGATGTAATGTAATGCTGTCCAGTTTATTTTATTTTATGTTGA 2755
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DB 785 TACATAGAAAAGATCTTGTATTATTTAAATGAGTTAAAGCTTGATTTCTTTGGT 844
QY 2931 CTGCAAGCTATCTGCCAGTTAATGCAATGCAACATTTTATGTCAGAAAACACA 2990
DB 845 CTGCAAGCTATCTGCCAGTTAATGCAATGCAACATTTTATGTCAGAAAACACA 904

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LOCUS	CN646545		
DEFINITION	ILLUMISEN MQC 26510 Katze_FEMR Macaca mulatta cDNA clone IB10W:8461 (Hs.1197922), mRNA sequence.		
ACCESSION	CN646545		
VERSION	CN646545.1	GI:47159988	
KEYWORDS	EST.		
SOURCE	Macaca mulatta (rhesus monkey)		
ORGANISM	Macaca mulatta		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Ceropithecidae; Cercopithecoinae; Macaca.		
AUTHORS	1 (bases 1 to 952) Magnes,C.L., Fellin,P.C., Thomas,M.J., Korzh,M.U., Agy,M.B., Prohl,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and Iadonato,S.P.		
TITLE	Analysis of the Macaca mulatta transcriptome and the sequence divergence between Macaca and human genome Biol. 6 (7), R60 (2005) 15998449		
JOURNAL	Contact: C. Magnes Illumigen Biosciences Inc. 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA Tel: 2063780400 Fax: 2063780408 Email: cmagnes@illumigen.com		
PUBMED	Sequenced on 2004.03.05. 790 Q20 bases. PCR primers FORWARD: CCCCTACTAAGGGAACAAA BACKWARD: CACTATAGGGCATTTGGTA Insert Length: 952 Std Error: 0.00 Plate: CL000176 row: G column: 12 Seq primer: CCCCTACTAAGGGAACAAA POLYA=Yes		
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Dd	128	CTGTGTCTTACTCTCCCCAAGAACAATGATTAGGAGAGAAATAAGACGCGGTAAAC	187
Oy	2278	AGTTATTGGCAAAAGCATGAAAGAGAGAACCTTGAAATTTTATTACTAGCTTGCTAC	2337
Dd	188	AGTTACTGGCAAAAGCATGAAAGAGAGAACCTTGAAATTTTATTACTAGCTTGCTAC	247

Qy	2338	CCACGATGAATTAACAACCTGTATCTGTGATATGACGCCGGGACAATATAGCCAGAGG	2397
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VERSION	1		
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ACCESSION	CNE44007		
VERSION	CNE44007.1		
KEYWORDS	GI:47157450		
ORGANISM	EST.		
SOURCE	Macaca mulatta (rhesus monkey)		
ORGANISM	Macaca mulatta		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
ORGANISM	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
ORGANISM	Cercopithecoidea; Cercopithecinae; Macaca.		
ORGANISM	1 (bases 1 to 955)		
ORGANISM	Magnus,C.B., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,		
ORGANISM	Prohl,S.C., Flitzdibon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and		
ORGANISM	Iadonato,S.P.		
ORGANISM	Analysis of the Macaca mulatta transcriptome and the sequence		
ORGANISM	divergence between Macaca and human		
ORGANISM	Genome Biol. 6 (7), R60 (2005)		
ORGANISM	15998449		
ORGANISM	Contact: C. Magnus		
ORGANISM	COMMENT		

Thu Mar 9 09:22:28 2006

us-10-071-645-3.rst

Page 12

[illegible]

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Qy	2278 AGTTATTCGCAAAAGCATGAAAAGAGAAGCATTGAAATTTATTACTAGCTGCTAC	2337
Dd	188 AGTTACTGCGAAAAGCATGAAAAGAGAAGCATTGAAATTTATTACTAGCTGCTAC	247
Qy	2338 CCACGATGAATTAACAACCTGTATCTGTATCAGCGCGGAGACAGATGAGCGAGG	2397
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Dd	425 TCTCAGTTGAGGCTATTTGTCAAAATTAATATCATTTCTTTTATATACGGTAGATAT	484
Qy	2576 GCGCAATTAATAGATCTCGAATTTTGAACCACTTAATGAAGCGGCAACACAGGCTTTGA	2635
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 ACCESSION CN803392.1 GI:47699368
 VERSION EST
 KEYWORDS Macaca mulatta (rhesus monkey)
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 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Cercopithecoidea; Cercopithecinae; Macaca.

REFERENCE 1 (bases 1 to 954)
 MAGNESS, C.L., FELLIN, P.C., THOMAS, M.J., KORTH, M.J., AGY, M.B.,
 PROLL, S.C., FITZGIBBON, M., SCHERER, C.A., MINER, D.G., KATZE, M.G. and
 IADONATO, S.P.
 Analysis of the Macaca mulatta transcriptome and the sequence
 divergence between Macaca and human
 Genome Biol. 6 (7), R60 (2005)
 15998449
 JOURNAL Contact: C. Magness
 PUBMED Illumigen Biosciences Inc.
 COMMENT 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
 Tel: 2063780400
 Fax: 2063780408
 Email: cmagness@illumigen.com
 Sequenced on 2004.04.03. 803 Q20 bases.
 PCR Primers
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 BACKWARD: CACTATAGGCGAATGCGTA
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 Site 2: Xho I; Created from Strategene ZAP-CDNA synthesis
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ORIGIN
 Query Match 24.4%; Score 779.4; DB 7; Length 954;
 Best Local Similarity 94.7%; Pred. No. 1.7e-145;
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Qy 421 CGAGCGCGCGCTGACCGCTGTCCGCGCGGGCGGGGACCGCGGTGAGAGAGCGCGCGCGCG 480
Db 421 CGAGCGCGCGCTGACCGCTGTCCGCGCGGGCGGGGACCGCGGTGAGAGAGCGCGCGCGCG 480
Qy 481 GAGCGCCCGGAGCGCGACCAATGTGAGAGGTGCTGCTTACCGGCGACGAGAGACTGAGCCCT 540
Db 481 GAGCGCCCGGAGCGCGACCAATGTGAGAGGTGCTGCTTACCGGCGACGAGAGACTGAGCCCT 540
Qy 541 TACGCGCGACGCGCGCGACGCTGAGGCCAGATCTTCTCGCGCGCTGACAGACACCAACAC 600
Db 541 TACGCGCGACGCGCGCGACGCTGAGGCCAGATCTTCTCGCGCGCTGACAGACACCAACAC 600
Qy 601 TTTCTTCGCGCGCGCGGAGAGACAGAGCGCGCGCGACAGCTGAGCGAGANTCGCGCGAGAG 660
Db 601 TTTCTTCGCGCGCGCGGAGAGACAGAGCGCGCGCGACAGCTGAGCGAGANTCGCGCGAGAG 660
Qy 661 CGGGGTGAGTTGCGCGGCGCGCTTGTCTGACACCGCCCTTTTCCCGCGCGCGGCGCTGAC 720
Db 661 CGGGGTGAGTTGCGCGGCGCGCTTGTCTGACACCGCCCTTTTCCCGCGCGCGGCGCTGAC 720
Qy 721 AAGGTTTCGCGAGGTTCTCCACCGCTGAGACCGCTTACAGACTGAGCAATCCCTTCTT 780
Db 721 AAGGTTTCGCGAGGTTCTCCACCGCTGAGACCGCTTACAGACTGAGCAATCCCTTCTT 780
Qy 781 GAGAGAAATGGGGGAGTCCCGGACGTGCGGGTCCGAGTGAAAGGGGTGCGAGAGACGCGTCC 840
Db 781 GAGAGAAATGGGGGAGTCCCGGACGTGCGGGTCCGAGTGAAAGGGGTGCGAGAGACGCGTCC 840
Qy 841 CCTAAGCCGAGATCCCGGCTGGGTGACCTTGGGGGCGTGGCGGCTTATAGAGACGATG 900
Db 841 CCTAAGCCGAGATCCCGGCTGGGTGACCTTGGGGGCGTGGCGGCTTATAGAGACGATG 900
Qy 901 GGGTCTCAACCGCGCGGAGAAAGTTTGTCTTTTAAATTTGGCCCCCGCCCGCTTTT 960
Db 901 GGGTCTCAACCGCGCGGAGAAAGTTTGTCTTTTAAATTTGGCCCCCGCCCGCTTTT 960
Qy 961 GGGCAGTGTAGTCAACGCTGCACTCGCTCCATTAACCTTGTGGGAGGGGGGCGCCAGAGAC 1020
Db 961 GGGCAGTGTAGTCAACGCTGCACTCGCTCCATTAACCTTGTGGGAGGGGGGCGCCAGAGAC 1020
Qy 1021 CCCGAGGGAGACGGGCTGGGAGACCTGCGTGGGAGAGATCCCATCTTCTGCGGGAAAGGCTAG 1080
Db 1021 CCCGAGGGAGACGGGCTGGGAGACCTGCGTGGGAGAGATCCCATCTTCTGCGGGAAAGGCTAG 1080
Qy 1081 GGTGTTCGGGTCGACGGGCTTTTCAATTTGATTTGGCTTGGAGAGGGGATTTTGCAGAGCC 1140
Db 1081 GGTGTTCGGGTCGACGGGCTTTTCAATTTGATTTGGCTTGGAGAGGGGATTTTGCAGAGCC 1140
Qy 1141 TGGGCGATCCGCGCGAGAGCTGAGAAACCCGAGAGAGCGAGAGCGAGAGAGGCTCCG 1200
Db 1141 TGGGCGATCCGCGCGAGAGCTGAGAAACCCGAGAGAGCGAGAGCGAGAGAGGCTCCG 1200
Qy 1201 AAGAGAGCTCCAGAGACGCGGGGAGCAATGAGGGGAGCCGACGCTGCGAGAGAGACTGA 1260
Db 1201 AAGAGAGCTCCAGAGACGCGGGGAGCAATGAGGGGAGCCGACGCTGCGAGAGAGACTGA 1260
Qy 1261 GACGCAAGGATGAGGGGAGAGGGGATACGCTGAGACCGAGGGGTGAGAGAGCCGAGCAA 1320
Db 1261 GACGCAAGGATGAGGGGAGAGGGGATACGCTGAGACCGAGGGGTGAGAGAGCCGAGCAA 1320
Qy 1321 AGCTCCGAGAGGGGAGCTGAAAGCCGAGAGACAGAGCCGAGAGACCGCCGTTTGGGGAGG 1380
Db 1321 AGCTCCGAGAGGGGAGCTGAAAGCCGAGAGACAGAGCCGAGAGACCGCCGTTTGGGGAGG 1380

Qy 1381 AAGCAGAAAGCGCGGAGAAACATTAAGGGCGACCGAGACCTTTAGACAGGAGAGAGAGAC 1440
Db 1381 AAGCAGAAAGCGCGGAGAAACATTAAGGGCGACCGAGACCTTTAGACAGGAGAGAGAGAC 1440
Qy 1441 CTGATTCGCGCTCCGCGCGCTTCGCGCGAGAGAGCATGAGAGGACCTGAGAAAGCGAGCT 1500
Db 1441 CTGATTCGCGCTCCGCGCGCTTCGCGCGAGAGAGCATGAGAGGACCTGAGAAAGCGAGCT 1500
Qy 1501 AAGTGAAGACGGTTAAGAGAGCGGAGGTTACCGCAATGTGTCCCTGCGAGGACCGAGAGG 1560
Db 1501 AAGTGAAGACGGTTAAGAGAGCGGAGGTTAAGGCAATGTGTCCCTGCGAGGAGCGAGAGG 1560
Qy 1561 AAGCTCTGACCTTGCAGAGCGGAGAGCGCGGGCGGCGGAGTCAGTGAGCGACAGGCT 1620
Db 1561 AAGCTCTGACCTTGCAGAGCGGAGAGCGCGGGCGGCGGAGTCAGTGAGCGACAGGCT 1620
Qy 1621 GGGAGAGGGCGCGCAGAGAGGGGCGCGCGCGCCAGGCGCAGGCTTAAACCCCGACCGCTGC 1680
Db 1621 GGGAGAGGGCGCGCAGAGAGGGGCGCGCGCGCCAGGCGCAGGCTTAAACCCCGACCGCTGC 1680
Qy 1681 GCGTCTGAGGAACCGGTTTGTGCGGTCCCTCCTGAGTTCCGCTCATCTCGCACCTAGCCT 1740
Db 1681 GCGTCTGAGGAACCGGTTTGTGCGGTCCCTCCTGAGTTCCGCTCATCTCGCACCTAGCCT 1740
Qy 1741 TGCACACCGGAGCTTGCCTCGGAGCTTACCTGAGGATCCCGAGACCCAGAAAGCTTTGGCTC 1800
Db 1741 TGCACACCGGAGCTTGCCTCGGAGCTTACCTGAGGATCCCGAGACCCAGAAAGCTTTGGCTC 1800
Qy 1801 CCTCTCTATCCAGACTTCAGACATTTCTGTCTAAATTAAGTGGCGCTGAGTGGGAGAGAG 1860
Db 1801 CCTCTCTATCCAGACTTCAGACATTTCTGTCTAAATTAAGTGGCGCTGAGTGGGAGAGAG 1860
Qy 1861 CCGGAGCAGTGCAGGCGCGCTGAGTGGAGAGAGGCGGTGGGTGGCGCTCTGTTC 1920
Db 1861 CCGGAGCAGTGCAGGCGCGCTGAGTGGAGAGAGGCGGTGGGTGGCGCTCTGTTC 1920
Qy 1921 TTTTCTCAGAAATGAGACCTGAGAGCGCAGCTGAGAGATTAAGGGGTGAGGCTTACAG 1980
Db 1921 TTTTCTCAGAAATGAGACCTGAGAGCGCAGCTGAGAGATTAAGGGGTGAGGCTTACAG 1980
Qy 1981 GAAAGCAGGAAAGGAGACCCCTGCGCAGGAGCGAGAGATGAGACTGTTTACCGCGAGTGA 2040
Db 1981 GAAAGCAGGAAAGGAGACCCCTGCGCAGGAGCGAGAGATGAGACTGTTTACCGCGAGTGA 2040
Qy 2041 GCGCTGCTCCCTGCGCTCTCTCTCTCCGACCTTCCACTGTGGGCAATAAGGAAATGTC 2100
Db 2041 GCGCTGCTCCCTGCGCTCTCTCTCTCCGACCTTCCACTGTGGGCAATAAGGAAATGTC 2100
Qy 2101 AAGAGCTCTGAGCTAGGCGCCGAGCGGCTCACCTCTCTTTTCCCGCTTTTGTGCAATT 2160
Db 2101 AAGAGCTCTGAGCTAGGCGCCGAGCGGCTCACCTCTCTTTTCCCGCTTTTGTGCAATT 2160
Qy 2161 GTTATTGAAGATGATGAGATTGATGACGTTGTAATAATATGACGACAGGACCTTCT 2220
Db 2161 GTTATTGAAGATGATGAGATTGATGACGTTGTAATAATATGACGACAGGACCTTCT 2220
Qy 2221 GGTGTCTAACTCCCGCAAGACATATGATTAAGGAGAGATTAAGAACCGCGGTAAAGT 2280
Db 2221 GGTGTCTAACTCCCGCAAGACATATGATTAAGGAGAGATTAAGAACCGCGGTAAAGT 2280
Qy 2281 TATTGGCAAAAAGCATGAAAAGAAAAGCACTTTGAAATTTTATTACTTACCTTGTACCCA 2340
Db 2281 TATTGGCAAAAAGCATGAAAAGAAAAGCACTTTGAAATTTTATTACTTACCTTGTACCCA 2340
Qy 2341 CGATGAATATCAACAACCTGTATCTGTGATCAGGCGGGAGACGATGAGGCGGAGAGAGG 2400
Db 2341 CGATGAATATCAACAACCTGTATCTGTGATCAGGCGGGAGACGATGAGGCGGAGAGAGG 2400
Qy 2401 AAGAGAGGAGGAGAGAGGCTTGGGCTCTCTGCAAAAATTAATAATTAATAATTAATA 2460
Db 2401 AAGAGAGGAGGAGAGAGGCTTGGGCTCTCTGCAAAAATTAATAATTAATAATTAATAATA 2460

Qy	2461	AATTTTAAAAATATATAAAATTCATATATACATATTAAGAAATTAAGAAAGCTCA	2520
Db	2461	AATTTTAAAAATATATAAAATTCATATATACATATTAAGAAATTAAGAAAGCTCA	2520
Qy	2521	GTTCGAGCTATTTGTCAAAAATTAATATCATTTCTTTATATATACGGTAATATATGGCA	2580
Db	2521	GTTCGAGCTATTTGTCAAAAATTAATATCATTTCTTTATATATACGGTAATATATGGCA	2580
Qy	2581	ATTATAGATCGGAAATTTTGAACAATTAAAGAGCGCAACACAGAGTTTTGAAGGT	2640
Db	2581	ATTATAGATCGGAAATTTTGAACAATTAAAGAGCGCAACACAGAGTTTTGAAGGT	2640
Qy	2641	TGGCAATCTTCGCGATTTGGCTGTCCCAATGTTTACATATTTAACTTTCGAAAG	2700
Db	2641	TGGCAATCTTCGCGATTTGGCTGTCCCAATGTTTACATATTTAACTTTCGAAAG	2700
Qy	2701	GTTCGAGCTATTTGTCAAAAATTAATATCATTTCTTTATATATACGGTAATATGGCA	2760
Db	2701	GTTCGAGCTATTTGTCAAAAATTAATATCATTTCTTTATATATACGGTAATATGGCA	2760
Qy	2761	GGATATCAAAAAATTCAGAAAAATCTCGATATATCTGTTTATTTTGGTCACT	2820
Db	2761	GGATATCAAAAAATTCAGAAAAATCTCGATATATCTGTTTATTTTGGTCACT	2820
Qy	2821	TTAAGATATACGGAATGTCTTTAAACAAGAGAACTTTTCTAAGAAATGATAC	2880
Db	2821	TTAAGATATACGGAATGTCTTTAAACAAGAGAACTTTTCTAAGAAATGATAC	2880
Qy	2881	AGAAAAAGATTTTATTTTAAATAGATGTGAAGCTTGTTTCTTTGTGTGCAAGCTA	2940
Db	2881	AGAAAAAGATTTTATTTTAAATAGATGTGAAGCTTGTTTCTTTGTGTGCAAGCTA	2940
Qy	2941	TTCTGCCAAGTAAATGCAAATGACACATTTTATATGTCAAAAAACAACAACAACA	3000
Db	2941	TTCTGCCAAGTAAATGCAAATGACACATTTTATATGTCAAAAAACAACAACAACA	3000
Qy	3001	CACACACACACACACACACGAAAAACAAGAAAAAATGCTTGAAGCTTTTCTAACTT	3060
Db	3001	CACACACACACACACACACGAAAAACAAGAAAAAATGCTTGAAGCTTTTCTAACTT	3060
Qy	3061	CCCCCTGACGTCTGTGTGTGAGCAGCTGTTTATTTCTCTAATATATATGTCAGTTAT	3120
Db	3061	CCCCCTGACGTCTGTGTGTGAGCAGCTGTTTATTTCTCTAATATATATGTCAGTTAT	3120
Qy	3121	CTCTTTATATGACCTGTAAAAAATGTATATCAAGAAGTCCAAATTTCTTGAATGCCAA	3180
Db	3121	CTCTTTATATGACCTGTAAAAAATGTATATCAAGAAGTCCAAATTTCTTGAATGCCAA	3180
Qy	3181	AGGCTTTTAA 3189	
Db	3181	AGGCTTTTAA 3189	

RESULT 2
US-10-198-846-11350
Sequence 11350, Application US/10198846
Publication No. US20030099974A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11350

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?      LENGTH: 1850
?      TYPE: DNA
?      ORGANISM: Homo sapiens
?      FEATURE:
?      NAME/KEY: misc_feature
?      LOCATION: 1, 26, 107, 1839, 1840, 1841, 1842, 1843, 1844, 1845, 1846
?      LOCATION: 1847, 1848, 1849, 1850
?      OTHER INFORMATION: n = A,T,C or G
US-10-198-846-11350

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Query Match	31.6%;	Score 1006.4;	DB 5;	Length 1850;
Best Local Similarity	99.6%;	Pred. No. 1.1e-213;		
Matches 1030; Conservative	0;	Mismatches 1;	Indels 3;	Gaps 2;

[illegible]

Qy	3056	AACTTCCCTCCCTGAGCTGTGTGTGAGACAGCCGTTTATTTCTCTAAATATATATGCAAT	3115
Db	1167	AACTTCCCTCCCTGAGCTGTGTGTGAGACAGCCGTTTATTTCTCTAAATATATATGCAAT	1266
Qy	3116	TTATCTCTTAAATGACGTGTAATAAATGTAATTCACAAGAGTGGCAAT-TCTTGAAT	3174
Db	1227	TTATCTCTTAAATGACGTGTAATAAATGTAATTCACAAGAGTGGCAATATCTTGAAT	1286
Qy	3175	GCCAAAGAGCTTTT	3188
Db	1287	GCCAAAGAGCAATTT	1300

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1 RESULT 3
2 US-09-820-649-25
3 Sequence 25, Application US/09820649
4 Publication No. US20030199683A1
5 GENERAL INFORMATION:
6 APPLICANT: Ruben et al
7 TITLE OF INVENTION: 83 Human Secreted Proteins
8 FILE REFERENCE: P2012P
9 CURRENT APPLICATION NUMBER: US/09/820,649
10 CURRENT FILING DATE: 2001-03-30
11 PRIOR APPLICATION NUMBER: US/09/236,557
12 PRIOR FILING DATE: 1999-01-26
13 PRIOR APPLICATION NUMBER: PCT/US98/15949
14 PRIOR FILING DATE: 1998-07-29
15 PRIOR APPLICATION NUMBER: 60/054,212
16 PRIOR FILING DATE: 1997-07-30
17 PRIOR APPLICATION NUMBER: 60/054,209
18 PRIOR FILING DATE: 1997-07-30
19 PRIOR APPLICATION NUMBER: 60/054,234
20 PRIOR FILING DATE: 1997-07-30
21 PRIOR APPLICATION NUMBER: 60/054,218
22 PRIOR FILING DATE: 1997-07-30
23 PRIOR APPLICATION NUMBER: 60/054,214
24 PRIOR FILING DATE: 1997-07-30
25 PRIOR APPLICATION NUMBER: 60/054,236
26 PRIOR FILING DATE: 1997-07-30
27 PRIOR APPLICATION NUMBER: 60/054,215
28 PRIOR FILING DATE: 1997-07-30
29 PRIOR APPLICATION NUMBER: 60/054,211
30 PRIOR FILING DATE: 1997-07-30
31 Remaining SEQ ID NOS: 353
32 NUMBER OF SEQ ID NOS: 353
33 SOFTWARE: PatentIn Ver. 2.0
34 SEQ ID NO 25

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? LENGTH: 1510
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: SITE
? LOCATION: (39)
? OTHER INFORMATION: n equals a,t,g, or c
US-09-820-649-25

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Query Match	31.4%;	Score 1002.4;	DB 3;	Length 1510;
Best Local Similarity	99.2%;	Pred. No. 7.5e-213;		
Matches 1030; Conservative	0;	Mismatches 1;	Indels 7;	Gaps 2

Qy	2158	GTTGTTATGGAAGATGATAGAAATGACGCGCTGAAAAATATGACCGACAGGACCT	221
Db	112	GTTGTTATGGAAGATGATAGAAATGACGCGCTGAAAAATATGACCGACAGGACCT	171
Qy	2218	CTGCGGTCTTAACTCCCCCAAGACAAATGATAGAGAGAAATTAAGACGCGGTAACT	227
Db	172	CTGCGGTCTTAACTCCCCCAAGACAAATGATAGAGAGAAATTAAGACGCGGTAACT	231
Qy	2278	AGTATATGGCAAAAAAGCATGAAAAAGAAAGCATTTGAATTATATCTAGCTTGCTAC	233
Db	232	AGTATATGGCAAAAAAGCATGAAAAAGAAAGCATTTGAATTATATCTAGCTTGCTAC	291

US-RESULT 4
 US-160-160-162-25
 Sequence 25, Application US/10160162
 Publication No. US20030166541A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: 83 Human Secreted Proteins
 FILE REFERENCE: P021P2
 CURRENT APPLICATION NUMBER: US/10/160,162
 CURRENT FILING DATE: 2002-06-04
 PRIOR APPLICATION NUMBER: 60/295,558
 PRIOR FILING DATE: 2001-06-05

[illegible]

Db	292	CCACGATGAAATCAACAACCTGTATCTGGTATCAGGCGGGAGACAGTATAGGCGAGAGG	351
Qy	2389	AGGAGAGAGAGAGAGAGAGAGGCTCTGGGCTCTCTGCAAAAATTAATAATAATAATA	2457
Db	352	AGGAGAGAGAGAGAGAGAGAGGCTCTGGGCTCTCTGCAAAAATTAATAATAATAATA	411
Qy	2458	TTAAATTTTAAATTAATTAATAATTCCTATATACATATTAAGAAATTAAGAAGTC	2517
Db	412	TTAAATTTTAAATTAATTAATAATTCCTATATACATATTAAGAAATTAAGAAGTC	471
Qy	2518	TCAGTGCACCTATTTGTCAAAATTAATAATTCATTTCTTTTATATACGGTGAATATGC	2577
Db	472	TCAGTGCACCTATTTGTCAAAATTAATAATTCATTTCTTTTATATACGGTGAATATGC	531
Qy	2578	GCAATTTATGATCTGGAATTTTGAACCACTTATGAAGCGGCAACACGAGTGTTTGAGG	2637
Db	532	GCAATTTATGATCTGGAATTTTGAACCACTTATGAAGCGGCAACACGAGTGTTTGAGG	591
Qy	2638	TGTTGGGCAATTCCTCGGTGATTTGGCTCTCCCAAGTTTGAATATTTAAATCTTGCANA	2697
Db	592	TGTTGGGCAATTCCTCGGTGATTTGGCTCTCCCAAGTTTGAATATTTAAATCTTGCANA	651
Qy	2698	ATGGTCTGTCGACCTGGATGAGAAAGCTGTCAGTTTATTTTTTTATGTTGTATC	2757
Db	652	ATGGTCTGTCGACCTGGATGAGAAAGCTGTCAGTTTATTTTTTTATGTTGTATC	711
Qy	2758	CTGGATGATGCAAAAAATTCAGAAAAATGATCTCTGAGATATCTCGTTTATTTGGTCA	2817
Db	712	CTGGATGATGCAAAAAATTCAGAAAAATGATCTCTGAGATATCTCGTTTATTTGGTCA	771
Qy	2818	TCTTTAAGATTTTCAGGAATGCTTTTAAACAAAGAGAACTTTCTAAGAAATGAT	2877
Db	772	TCTTTAAGATTTTCAGGAATGCTTTTAAACAAAGAGAACTTTCTAAGAAATGAT	831
Qy	2878	CATGAAAAAATTTTATTTTAAATGATGCTTAAAGCTTGTTCTTTGTCGCAAG	2937
Db	832	CATGAAAAAATTTTATTTTAAATGATGCTTAAAGCTTGTTCTTTGTCGCAAG	891
Qy	2938	CTATCTGCCCAAGTTATATGCAATATGACACATTTTATTTATGTCAGAAAA-----ACACAC	2991
Db	892	CTATCTGCCCAAGTTATATGCAATATGACACATTTTATTTATGTCAGAAAAACACACACAC	951
Qy	2992	AC	3051
Db	952	AC	1011
Qy	3052	TCTTAATCTCCCTTCGAGCTGTGTGTGAGACGCGTTTATTTCTTAATATATATGT	3111
Db	1012	TCTTAATCTCCCTTCGAGCTGTGTGTGAGACGCGTTTATTTCTTAATATATATGT	1071
Qy	3112	CAGTTTATCTCTTTAATGACCTGTAAATAAATATGTAATCAACAAGTGCACAAAT-TCGTG	3170
Db	1072	CAGTTTATCTCTTTAATGACCTGTAAATAAATATGTAATCAACAAGTGCACAAATATCTTG	1131
Qy	3171	AAATGCCAAAGAGCTTTT 3188	
Db	1132	AAATGCCAAAGAGCATTT 1149	
RESULT 5			
US-10-936-773-25			
Sequence 25, Application US/10936773			
Publication No. US2005037467A1			
GENERAL INFORMATION:			
APPLICANT: Ruben et al.			
TITLE OF INVENTION: 83 Human Secreted Proteins			
FILE REFERENCE: P2012P2			
CURRENT FILING DATE: 2004-09-09			
PRIORITY APPLICATION NUMBER: US/10/160,162			
PRIORITY FILING DATE: 2002-06-04			
PRIORITY APPLICATION NUMBER: 60/295,558			

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? PRIOR FILING DATE: 2001-06-05
? PRIOR APPLICATION NUMBER: 09/236,557
? PRIOR FILING DATE: 1999-01-26
? PRIOR APPLICATION NUMBER: PCT/US98/15949
? PRIOR FILING DATE: 1998-07-29
? PRIOR APPLICATION NUMBER: 60/054,212
? PRIOR FILING DATE: 1997-07-30
? PRIOR APPLICATION NUMBER: 60/054,209
? PRIOR FILING DATE: 1997-07-30
? PRIOR APPLICATION NUMBER: 60/054,234
? PRIOR FILING DATE: 1997-07-30
? PRIOR APPLICATION NUMBER: 60/054,218
? PRIOR FILING DATE: 1997-07-30
? PRIOR APPLICATION NUMBER: 60/054,214
? PRIOR FILING DATE: 1997-07-30
? PRIOR APPLICATION NUMBER: 60/054,236
? PRIOR FILING DATE: 1997-07-30
? Remaining Filer ID Application data removed - See File Wrapper or PALM
? NUMBER OF SEQ ID NOS: 353
? SOFTWARE: Patentin Ver. 2.0
? SEQ ID NO 25
? LENGTH: 1510
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: SITE
? LOCATION: (39)
? OTHER INFORMATION: n equals a,t,g, or c
? JS-10-936-773-25

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Query Match	31.4%;	Score 1003.4;	DB 8;	Length 1510;
Best Local Similarity	99.2%;	Pred. No. 7.5e-213;		
Matches 1030; Conservative	0;	Mismatches 1;	Indels 7;	Gaps 2

Qy	2758	TTTGAGTGTCAAAAAATTCAGAAATGATCTCTGATGATTCGTGTTATTTTGATCA	2817
Db	712	CTTGAGTGTCAAAAAATTCAGAAATGATCTCTGATGATTCGTGTTATTTTGATCA	771
Qy	2818	TCTTAGAATATATCGAAGATGTGTTAAAAACAAGAGAACTTTCTAAGAAATGATG	2877
Db	772	TCTTAGAATATATCGAAGATGTGTTAAAAACAAGAGAACTTTCTAAGAAATGATG	831
Qy	2878	CATGAAAAAGATTTTATTTTAAATGATGTTAAAGCTGTGTTCTTGTGTCGCAAG	2937
Db	832	CATGAAAAAGATTTTATTTTAAATGATGTTAAAGCTGTGTTCTTGTGTCGCAAG	891
Qy	2938	CTATGTGCCCCAAGTTATGCAAAATGACACATTTTATATGTGACAAAA-----ACAC	2991
Db	892	CTATGTGCCCCAAGTTATGCAAAATGACACATTTTATATGTGACAAAAACAACACAC	951
Qy	2992	ACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA	3051
Db	952	ACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA	1011
Qy	3052	TTCTAACTTCCCTTGACGTCTGTGTGTGAGACGCTGTTATTTCTCTAAATATATGT	3111
Db	1012	TTCTAACTTCCCTTGACGTCTGTGTGTGAGACGCTGTTATTTCTCTAAATATATGT	1071
Qy	3112	CAGTTTATTTCTGTTTATGACCTGTAAAAAATGTATACACAAGTGCCTAAT-TCTTG	3170
Db	1072	CAGTTTATTTCTGTTTATGACCTGTAAAAAATGTATACACAAGTGCCTAATATCTTG	1131
Qy	3171	AAATGCCAAAGGCTTTT 3188	
Db	1132	AAATGCCAAAGGCAATTT 1149	

RESULT 6
US-10-723-860-7058/c
; Sequence 7058, Application US/10723860
; Publication No. US20040253606A1

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APPLICANT: ziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
FILE REFERENCE: 05889, 0193, NPL001
CURRENT APPLICATION NUMBER: US/0-723, 860
PRIOR FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/423, 739
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7058
LENGTH: 2058
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1952)..(1952)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2033)..(2033)
OTHER INFORMATION: n is a, c, g, or t
US-10-723-860-7058

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	Query Match	31.4%	Score 1002.4	DB 8	Length 2056
	Best Local Similarity	99.2%	Pred. No. 8.8e-213		
	Matches 1030	Conservative	0	Mis. 1	Indels 7, Gaps 2
QY	2158	GTTGTATTGAGATGATGAGATTGATGAGCTGCGTCAAAAATATGACCGACGACGACT	2217		
Qb	1798	GTTGTATTGAGATGATGAGATTGATGAGCTGCTCGTCAAAAATATGACCGACGACGACT	1733		

QY 2218 CTTGCTGCTTAACTCCCGAAGACATGATTAGGAGAGATTAAGACCGCGCTAAC 2277
 DB 1738 CTTGCTGCTTAACTCCCGAAGACATGATTAGGAGAGATTAAGACCGCGCTAAC 1679
 QY 2278 AGTTATTTGGCAAAAGCATGAAAAGAGAAAGCACTTTGAAATTTTATTAAGTCTGCTAC 2337
 DB 1678 AGTTATTTGGCAAAAGCATGAAAAGAGAAAGCACTTTGAAATTTTATTAAGTCTGCTAC 1619
 QY 2338 CCAGCATGAAATCAACACCTGTATCTGTATACAGCCCGGAGACAGATGAGCGAGAG 2397
 DB 1618 CCAGCATGAAATCAACACCTGTATCTGTATACAGCCCGGAGACAGATGAGCGAGAG 1559
 QY 2398 AGAGAGAGAGAGAGAGAGAGCTCTGAGCTCTCTGCAAAAAATAAAAATAAAAATAAA 2457
 DB 1558 AGAGAGAGAGAGAGAGAGAGCTCTGAGCTCTCTGCAAAAAATAAAAATAAAAATAAA 1499
 QY 2458 TAAATTTTAAAAAT 2517
 DB 1498 TAAATTTTAAAAAT 1439
 QY 2518 TCAGTTCAGCTATTTTGTCAAAATTAATATCAATTTCTTTTATATATATATATATATAT 2577
 DB 1438 TCAGTTCAGCTATTTTGTCAAAATTAATATCAATTTCTTTTATATATATATATATATAT 1379
 QY 2578 GCATTTAT 2637
 DB 1378 GCATTTAT 1319
 QY 2638 TGTGGCACTTCTGCTGATTTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2697
 DB 1318 TGTGGCACTTCTGCTGATTTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1259
 QY 2698 ATGTTCTGTGCACTTGTGATGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2757
 DB 1258 ATGTTCTGTGCACTTGTGATGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1199
 QY 2758 CTTGATGTACAAAAAATTCAGAAAAATGATCTCTGTATATATATATATATATATATATAT 2817
 DB 1198 CTTGATGTACAAAAAATTCAGAAAAATGATCTCTGTATATATATATATATATATATATAT 1139
 QY 2818 TCTTTAGATGTATCAGAAATGCTTTTAAAAAAGAAAGAACTTTCTAAGATGATA 2877
 DB 1138 TCTTTAGATGTATCAGAAATGCTTTTAAAAAAGAAAGAACTTTCTAAGATGATA 1079
 QY 2878 CATAGAAAAGATTTTATTTTAAAAATGATGTATGATGCTGCTGCTGCTGCTGCTGCTGCT 2937
 DB 1078 CATAGAAAAGATTTTATTTTAAAAATGATGTATGATGCTGCTGCTGCTGCTGCTGCTGCT 1019
 QY 2938 CTATCTGCGCAAGTTAATGCAAAATGAGACATTTTATATATATATATATATATATATAT 2991
 DB 1018 CTATCTGCGCAAGTTAATGCAAAATGAGACATTTTATATATATATATATATATATATAT 959
 QY 2992 ACAAC 3051
 DB 958 ACAAC 899
 QY 3052 TTTCTAACCTTCCCTTGCAGCTGCTGTGTGAGCAAGCTGCTGCTGCTGCTGCTGCTGCT 3111
 DB 898 TTTCTAACCTTCCCTTGCAGCTGCTGTGTGAGCAAGCTGCTGCTGCTGCTGCTGCTGCT 839
 QY 3112 CAGTTTATCTCTTTAATGACTGTAATAAAATATATATATATATATATATATATATATAT 3170
 DB 838 CAGTTTATCTCTTTAATGACTGTAATAAAATATATATATATATATATATATATATATAT 779
 QY 3171 AAATGCCAAAAGGCTTTT 3188
 DB 778 AAATGCCAAAAGGCTTTT 761

GENERAL INFORMATION:
 APPLICANT: Dai, Hongyue
 APPLICANT: He, Yudong
 APPLICANT: Linley, Peter
 APPLICANT: Mao, Mao
 APPLICANT: Robert, Chris
 APPLICANT: Van 't Veer, Laura
 APPLICANT: Van de Vijver, Marc
 TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
 FILE REFERENCE: 9301-175-999
 CURRENT FILING DATE: 2002-06-14
 PRIOR FILING DATE: 2002-05-14
 NUMBER OF SEQ ID NOS: 2699
 SEQ ID NO 1796
 LENGTH: 1321
 TYPE: DNA
 ORGANISM: Homo sapiens
 PUBLICATION INFORMATION:
 DATABASE ACCESSION NUMBER: NM 018584
 DATABASE ENTRY DATE: 2001-06-18
 US-10-172-118-1796

Query Match 31.4%; Score 1000.8; DB 6; Length 1321;
 Best Local Similarity 99.1%; Pred. No. 1.6e-212;
 Matches 1029; Conservative 0; Mismatches 2; Indels 7; Gaps 2;

QY 2158 GTTGTATTGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2217
 DB 33 GTTGTATTGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 92
 QY 2218 CTTGCTGCTTAACTCCCGAAGACATGATTAGGAGAGATTAAGACCGCGCTAAC 2277
 DB 93 CTTGCTGCTTAACTCCCGAAGACATGATTAGGAGAGATTAAGACCGCGCTAAC 152
 QY 2278 AGTTATTTGGCAAAAGCATGAAAAGAGAAAGCACTTTGAAATTTTATTAAGTCTGCTAC 2337
 DB 153 AGTTATTTGGCAAAAGCATGAAAAGAGAAAGCACTTTGAAATTTTATTAAGTCTGCTAC 212
 QY 2338 CCAGCATGAAATCAACACCTGTATCTGTATACAGCCCGGAGACAGATGAGCGAGAG 2397
 DB 213 CCAGCATGAAATCAACACCTGTATCTGTATACAGCCCGGAGACAGATGAGCGAGAG 212
 QY 2398 AGAGAGAGAGAGAGAGAGAGCTCTGAGCTCTCTGCAAAAAATAAAAATAAAAATAAA 2457
 DB 273 AGAGAGAGAGAGAGAGAGAGCTCTGAGCTCTCTGCAAAAAATAAAAATAAAAATAAA 332
 QY 2458 TAAATTTTAAAAAT 2517
 DB 333 TAAATTTTAAAAAT 392
 QY 2518 TCAAGTTCAGCTATTTGTCAAAATTAATATATATATATATATATATATATATATATAT 2577
 DB 393 TCAAGTTCAGCTATTTGTCAAAATTAATATATATATATATATATATATATATATATAT 452
 QY 2578 GCAATTTAT 2637
 DB 453 GCAATTTAT 512
 QY 2638 TGTGGCACTTCTGCTGATTTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2697
 DB 513 TGTGGCACTTCTGCTGATTTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 572
 QY 2698 ATGTTCTGTGCACTTGTGATGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2757
 DB 573 ATGTTCTGTGCACTTGTGATGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 632
 QY 2758 CTTGATGTACAAAAAATTCAGAAAAATGATCTCTGTATATATATATATATATATATATAT 2817
 DB 633 CTTGATGTACAAAAAATTCAGAAAAATGATCTCTGTATATATATATATATATATATATAT 692

QY 2818 TCTTTAGAGTTATCGAGATGCTTTTAAACAGAGAGAACTTTCTAAGAAATGA 2877
 Db 693 TCTTTAGAGTTATCGAGATGCTTTTAAACAGAGAGAACTTTCTAAGAAATGA 752
 QY 2878 CATAGAAAAGATTTTATTTTAAATGAGTTGTAAGCTTGTCTTTCTGCTCCAG 2937
 Db 753 CATAGAAAAGATTTTATTTTAAATGAGTTGTAAGCTTGTCTTTCTGCTCCAG 812
 QY 2938 CTATCTGCCCAAGTTATGCAATGAGACATTTTATATGCAAAA-----ACAC 2991
 Db 813 CTATCTGCCCAAGTTATGCAATGAGACATTTTATATGCAAAAACACACACAC 872
 QY 2992 AC 3051
 Db 873 AC 932
 QY 3052 TTCTTAACCTCCCTGCACTGTGTGTGAGACGCTGTTATTTCTTAATATATGT 3111
 Db 933 TTCTTAACCTCCCTGCACTGTGTGTGAGACGCTGTTATTTCTTAATATATGT 992
 QY 3112 CAGTTTATCTCTTTATGACTGTAAATAATGTATCAAGAGTCCCAAT-TCCTTG 3170
 Db 993 CAGTTTATCTCTTTATGACTGTAAATAATGTATCAAGAGTCCCAATATCTTG 1052
 QY 3171 AAATGCCAAAAGGCTTTT 3188
 Db 1053 AAATGCCAAAAGGCTTTT 1070

RESULT 8

US-10-342-887-1796
 ; Sequence 1796, Application US/10342887
 ; Publication No. US20040058340A1
 GENERAL INFORMATION:
 ; APPLICANT: Dai, Hongyue
 ; APPLICANT: He, Yudong
 ; APPLICANT: Lindeley, Peter S.
 ; APPLICANT: Mao, Mao
 ; APPLICANT: Roberts, Christopher J.
 ; APPLICANT: Van 't Veer, Laura Johanna
 ; APPLICANT: Van de Vijver, Marc J.
 ; APPLICANT: Bernards, Rene
 TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
 ; FILE REFERENCE: 9301-188-999
 ; CURRENT APPLICATION NUMBER: US/10/342,887
 ; PRIOR FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: 60/298,918
 ; PRIOR FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: 60/380,710
 ; PRIOR FILING DATE: 2002-05-14
 ; PRIOR APPLICATION NUMBER: 10/172,118
 ; PRIOR FILING DATE: 2002-06-14
 ; NUMBER OF SEQ ID NOS: 2639
 ; SEQ ID NO 1796
 ; LENGTH: 1321
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-342-887-1796

Query Match 31.4%; Score 1000.8; DB 7; Length 1321;
 Best Local Similarity 99.1%; Pred. No. 1.6e-212;
 Matches 1029; Conservative 0; Mismatches 2; Indels 7; Gaps 2;

QY 2158 GTTGTATTGAAGATGATGATTTGATGCTGTGTAATAATGACGACAGAGCACT 2217
 Db 33 GTTGTATTGAAGATGATGATTTGATGCTGTGTAATAATGACGACAGAGCACT 92
 QY 2218 CTTGATGTCTAATCTCCCAAGACATGATTAAGGAGAGATTAAGAACGCGGTAA 2277
 Db 93 CTTGATGTCTAATCTCCCAAGACATGATTAAGGAGAGATTAAGAACGCGGTAA 152
 QY 2278 AGTTATGGCAAAAAGCATGAAAGAGAAAGCACTTTGAAATTTACTAGCTGTAC 2337

Db 153 AGTTATGGCAAAAAGCATGAAAGAGAAAGCACTTTGAAATTTACTAGCTGTAC 212
 QY 2338 CCAGATGAAATCAACAACCTGATCTGTATCAGGCGGAGACAGATGAGCGAGAG 2397
 Db 213 CCAGATGAAATCAACAACCTGATCTGTATCAGGCGGAGACAGATGAGCGAGAG 272
 QY 2398 AG 2457
 Db 273 AG 332
 QY 2458 TAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2517
 Db 333 TAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 392
 QY 2518 TCAGTTGACGCTATTTGCAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 2577
 Db 393 TCAGTTGACGCTATTTGCAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 452
 QY 2578 GCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2637
 Db 453 GCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 512
 QY 2638 TGTGGCACTCTTGGCTGATTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2697
 Db 513 TGTGGCACTCTTGGCTGATTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 572
 QY 2698 ATGGTTCTGTGCACTTGAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 2757
 Db 573 ATGGTTCTGTGCACTTGAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 632
 QY 2758 CTTGATGTAACAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2817
 Db 633 CTTGATGTAACAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 692
 QY 2818 TCTTTAGAGTTATCGAGATGCTTTTAAACAGAGAGAACTTTCTAAGAAATGA 2877
 Db 693 TCTTTAGAGTTATCGAGATGCTTTTAAACAGAGAGAACTTTCTAAGAAATGA 752
 QY 2878 CATAGAAAAGATTTTATTTTAAATGAGTTGTAAGCTTGTCTTTCTGCTCCAG 2937
 Db 753 CATAGAAAAGATTTTATTTTAAATGAGTTGTAAGCTTGTCTTTCTGCTCCAG 812
 QY 2938 CTATCTGCCCAAGTTATGCAATGAGACATTTTATATGCAAAA-----ACAC 2991
 Db 813 CTATCTGCCCAAGTTATGCAATGAGACATTTTATATGCAAAAACACACACAC 872
 QY 2992 AC 3051
 Db 873 AC 932
 QY 3052 TTCTTAACCTCCCTGCACTGTGTGTGAGACGCTGTTATTTCTTAATATATGT 3111
 Db 933 TTCTTAACCTCCCTGCACTGTGTGTGAGACGCTGTTATTTCTTAATATATGT 992
 QY 3112 CAGTTTATCTCTTTATGACTGTAAATAATGTATCAAGAGTCCCAAT-TCCTTG 3170
 Db 993 CAGTTTATCTCTTTATGACTGTAAATAATGTATCAAGAGTCCCAATATCTTG 1052
 QY 3171 AAATGCCAAAAGGCTTTT 3188
 Db 1053 AAATGCCAAAAGGCTTTT 1070

RESULT 9

US-10-956-157-2260/C
 ; Sequence 2260, Application US/10956157
 ; Publication No. US20050118625A1
 GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Wyeth, William
 TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
 ; FILE REFERENCE: 031896-043000 (AM 101081)

Qy	2638	IGTGGCATTCTTCGGCTGATTTGGCTGTCCCAATGTTAACTATTTAAATCTTGCAGAA	2697
Dp	809	TGTTGGCATTCTTCGGCTGATTTGGCTGTCCCAATGTTAACTATTTAAATCTTGCAGAA	750
Qy	2698	ATGGTTCGGGCACTTGGATGTGAATGCAATGCTGTCAAGTTTATTTTTTAAATGTGTATTC	2755
Dp	749	ATGGTTCGGGCACTTGGATGTGAATGCAATGCTGTCAAGTTTATTTTTTAAATGTGTATTC	690
Qy	2758	CTTGGATGTCAAAAAATTCAGAAAAATATCTCTGTAGATATTCGTTTATTTTGGTCA	2817
Dp	689	CTTGGATGTCAAAAAATTCAGAAAAATATCTCTGTAGATATTCGTTTATTTTGGTCA	630
Qy	2818	TCTTTAAGAAGTTTCAAGAAATGTGTTTAAACAAGAAAGAACTTTTCTAAGAAATGATA	2877
Dp	629	TCTTTAAGAAGTTTCAAGAAATGTGTTTAAACAAGAAAGAACTTTTCTAAGAAATGATA	570
Qy	2878	CATGAAAAAGTTTTTATTTTAAAAAGAATTGAAGCTGTGTCTTGTGTGTGAAG	2933
Dp	569	CATGAAAAAGTTTTTATTTTAAAAAGAATTGAAGCTGTGTCTTGTGTGTGAAG	510
Qy	2938	CTATCTGCCCAAGTTAATGCAATGGAACAATTTTTTATGTAGAGAAA-----ACACAC	2992
Dp	509	CTATCTGCCCAAGTTAATGCAATGGAACAATTTTTTATGTAGAGAAAACAACAACACAC	450
Qy	2992	AC	3055
Dp	449	AC	390
Qy	3052	TTCCTAACTTCCCTCGACATCTGTGTGTGACGACCTGTTATTTCTCTAAATTTATGT	3111
Dp	389	TTCCTAACTTCCCTCGACATCTGTGTGTGACGACCTGTTATTTCTCTAAATTTATGT	330
Qy	3112	CAGTTATTTCTTTAATGACACTGAAAAAATGTATATCAACAAGTGTCCAAAT-TCTTG	3170
Dp	329	CAGTTATTTCTTTAATGACACTGAAAAAATGTATATCAACAAGTGTCCAAATATCTTG	270
Qy	3171	AAATGCCAAAAGCTTTT 3188	
Dp	269	AAATGCCAAAAGCAATTT 252	

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RESULT 11
US-10-765-700-70
Sequence 70, Application US/10765700
Publication No. US20050130171A1
GENERAL INFORMATION:
APPLICANT: Loring, Jeanne F.
APPLICANT: Tingley, Debora M.
APPLICANT: Edwards, Carla M.
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
FILE REFERENCE: PA-0024 US
CURRENT APPLICATION NUMBER: US/10/765,700
CURRENT FILING DATE: 2004-01-26
PRIOR APPLICATION NUMBER: US/09/566,921
PRIOR FILING DATE: PRIORT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL Program
SEQ ID NO 70
LENGTH: 1876
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 234151.1
FEATURE:
NAME/KEY: unsure
LOCATION: 1360, 1362-1391, 1864
OTHER INFORMATION: a, t, c, g, or other
US-10-765-700-70

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Query Match	30.2%;	Score 963.8;	DB 9;	Length 1876;
Best Local Similarity	96.5%;	Pred. No. 3.4e-204;		
Matches 1004; Conservative	0;	Mismatches 27;	Indels 9;	Gaps 3


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Db 508 GCGCCCGACCCCAACCCGCTAACCTTATCCGCGCGGACGAAAAACGCGATCGAAAAA 449
Qy 471 GCGCCCGCGGAGCGCCCGGACCGGACCAATGTCGGAAGTCTGCTTCCCTTACGGCGACGAA 530
Db 448 GCGCGGCGGAAACCCCGGACCGGACCAATGTCGGAAGTCTGCTTCCCTTACGGCGACGAA 389
Qy 531 GGTGAGCCCTTACGCGGAGCGCGGACGCGTGGAGCGAGATCTTCTCTCCCTCGCGAG 590
Db 388 ACTAAACCCCTTACGCGGAGCGCGGACGCGTGGAGCGAGATCTTCTCTCCCTCGCGAG 329
Qy 591 CACCAACAACTTCTTCCGCGCGCGGCGAGACAGACCGCGCGGACGCGGAGCGAGATCG 650
Db 328 CACCAACAACTTCTTCCGCGCGCGGCGAGACAGACCGCGCGGACGCGGAGCGAGATCG 269
Qy 651 CCGGAGCAGCGGCGGAGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 710
Db 268 CCGAAGCAAAAGAAATTAATTCGCGACCCCTTATCTAACACCCCTTTTCCGCGCG 209
Qy 711 CCGGCTGAAAGAGGTTGCGGAGGTCTCCGACCCGCGTGAAGCGCGTGAAGCGAG 770
Db 208 CGACCTAAACAAATTAATTCGAAATCTCCGACCTGCACTAACGAAATCGCAA 149
Qy 771 ATCCCTTCTGCAAAATGCGGAGATCCGCACTGCGGAGTCCGCGTGAAGCGGTCGAG 830
Db 148 ATCCCTTCTGCAAAATTAATTAATTCGCGACCTGCACTAACGAAATCGCAA 89
Qy 831 AACGCGTCCCTTAAGCGGATCCCGGCTGGGTCAACCTGGGGGGGTCGCGGCTTGA 890
Db 88 AACGCGTCCCTTAAGCGGATCCCGGCTGGGTCAACCTGGGGGGGTCGCGGCTTGA 29
Qy 891 CAGCAGCTGGGGGTCCTCAACCCGCGG 917
Db 28 CAAACAATAAAATCTCAACCCGCGG 2

RESULT 14
US-10-363-345A-29798
; Sequence 29798, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363.345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 29798
; LENGTH: 869
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 29798
US-10-363-345A-29798

Query Match 18.3%; Score 583.8; DB 8; Length 869;
Best Local Similarity 79.6%; Pred. No. 1.4e-119;
Matches 690; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

Qy 51 TCTGCTCTCCCGAAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 110
Db 2 TCTACTCTCCCGAAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 61
Qy 111 CCGGGGTCGCGCTCTCCCGGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 170
Db 62 CCGAAATATCGCTCTCCGATCCCGGCTCTCCGAAATATCGCGCGCGCGCGCGCGCGCG 121
Qy 171 CGGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 230
Db 122 CGACTCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 181
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Qy 231 GTCTGCTCTCCCGAAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 290
Db 182 ATCTACTCTCCCGAAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 241
Qy 291 CCGAAGCGCGCGCTCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 350
Db 242 CGAAGCGCGCGCTCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 301
Qy 351 TCCCGCGCGCTCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 410
Db 302 TCCCGCGCGCTCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 361
Qy 411 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 470
Db 362 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 421
Qy 471 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 530
Db 422 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 481
Qy 531 GGTGAGCCCTTACGCGGAGCGCGGACGATGTCGGAAGTCTGCTTCCCTTACGGCGAG 590
Db 482 ACTAAACCCCTTACGCGGAGCGCGGACGATGTCGGAAGTCTGCTTCCCTTACGGCGAG 541
Qy 591 CACCAACAACTTCTTCCGCGCGCGGCGAGACAGACCGCGCGGACGCGGAGCGAGATCG 650
Db 542 CACCAACAACTTCTTCCGCGCGCGGCGAGACAGACCGCGCGGACGCGGAGCGAGATCG 601
Qy 651 CCGGAGCAGCGGCGGAGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 710
Db 602 CCGAAGCAAAAGAAATTAATTCGCGACCCCTTATCTAACACCCCTTTTCCGCGCG 661
Qy 711 CCGGCTGAAAGAGGTTGCGGAGGTCTCCGACCCGCGTGAAGCGCGTGAAGCGAG 770
Db 662 CGACCTAAACAAATTAATTCGAAATCTCCGACCTGCACTAACGAAATCGCAA 721
Qy 771 ATCCCTTCTGCAAAATGCGGAGATCCGCACTGCGGAGTCCGCGTGAAGCGGTCGAG 830
Db 722 ATCCCTTCTGCAAAATTAATTAATTCGCGACCTGCACTAACGAAATCGCAA 781
Qy 831 AACGCGTCCCTTAAGCGGATCCCGGCTGGGTCAACCTGGGGGGGTCGCGGCTTGA 890
Db 782 AACGCGTCCCTTAAGCGGATCCCGGCTGGGTCAACCTGGGGGGGTCGCGGCTTGA 841
Qy 891 CAGCAGCTGGGGGTCCTCAACCCGCGG 917
Db 842 CAAACAATAAAATCTCAACCCGCGG 868

RESULT 15
US-10-363-483A-29797/c
; Sequence 29797, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363.483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 29797
; LENGTH: 869
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 29797
US-10-363-483A-29797
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Query Match 18.3%; Score 583.8; DB 9; Length 869;
 Best Local Similarity 79.6%; Pred. No. 1.4e-119;
 Matches 690; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

Qy 51 TCTGCTCCCGAACCAGGCGCGCCCGCCGACTGCGCGAGACCGAGCCCGCCGCTC 110
 Db 868 TCTACTCCCGAACCAGGCGCGCCCGCCGACTGCGCGAGACCGAGCCCGCCGCTC 809
 Qy 111 CGGAGGTCGCGCTCTCGGTCGCGCGCTCGAGGCTCGAGGAGACGTCCTCCCTCC 170
 Db 808 CGGAATACGCGCTCTCGATCCCGCGCTCGGAATCGCAAAAAGTCTCTCCCTCC 749
 Qy 171 CGGCTCGGCG 230
 Db 748 CGACTCGGAGACCG 689
 Qy 231 GTCCTGCTCGCTCTGCGCGAGACGAGCCACTGCGCGCGCGCGCGCGCGCGCGCG 290
 Db 688 ATCTACTCTGCTCTGAGAAACAAACGACTGCGCGCGCGCGCGCGCGCGCGCG 629
 Qy 291 CGGAGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 350
 Db 628 CGGAGCGCGAGCGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 569
 Qy 351 TCCCTCGGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 410
 Db 568 TCCCTCGAGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 509
 Qy 411 GCGCCCG 470
 Db 508 GCGCCCGAGCCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 449
 Qy 471 CGCGCGCGCGAGCG 530
 Db 448 CGCGCGCGAGAAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 389
 Qy 531 GCTGAGCG 590
 Db 388 ACTAAACCGCTACGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 329
 Qy 591 CACGAAACCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 650
 Db 328 CACGAAACCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 269
 Qy 651 CGGAGCGAGCG 710
 Db 268 CGGAAACGAAATTAATTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 209
 Qy 711 CGGCTGAAACAGGCTTCGCGAGCTTCGACCGCGCGCGCGCGCGCGCGCGCG 770
 Db 208 GAGCTTAACGAAATTAATTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 149
 Qy 771 ATCTCTTCTGCGAGATTCGCGAGATTCGCGAGATTCGCGAGATTCGCGAG 830
 Db 148 ATCTCTTCTGCGAGATTCGCGAGATTCGCGAGATTCGCGAGATTCGCGAG 89
 Qy 831 AACGGTCCCTTAAGCGGATTCGCGAGATTCGCGAGATTCGCGAGATTCGCGAG 890
 Db 88 AACGGTCCCTTAAGCGGATTCGCGAGATTCGCGAGATTCGCGAGATTCGCGAG 29
 Qy 891 CAGCAGCTGAGGCTTCGACCGCGCG 917
 Db 28 CAGCAGCTAAGATTCGACCGCGCG 2

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 22:09:41 ; Search time 990.945 Seconds
(without alignments)
7425.207 Million cell updates/sec

Title: US-10-071-645-3

Sequence: 1ccccccccccccccgcgc.....gaatgcacaaagccttta 3189

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 767375 seqs, 115364844 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA_New:
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2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	399.7	12.5	417	US-09-978-360A-155	Sequence 155, App
2	77.2	2.3	78	US-10-310-810A-8438	Sequence 8438, App
3	74.6	2.3	687411	US-10-310-773-26	Sequence 26, App1
4	70.2	2.2	1557	US-10-996-217A-6	Sequence 6, App1
5	70.2	2.2	16917	US-11-124-367A-5000	Sequence 5000, App
6	69	2.2	3167	US-09-925-065A-21764	Sequence 21764, App
7	68.2	2.1	2562	US-10-909-125-837	Sequence 533, App
8	68.2	2.1	4745	US-10-909-125-837	Sequence 837, App
9	67.8	2.1	2196	US-11-052-554A-539	Sequence 539, App
10	67.6	2.1	10524	US-11-075-185-37	Sequence 37, App1
11	67.6	2.1	16082	US-10-995-561-13485	Sequence 13485, App
12	67.6	2.1	23894	US-10-995-561-13320	Sequence 13320, App
13	67.6	2.1	78869	US-11-075-185-1	Sequence 1, App1
14	67.6	2.1	26868	US-10-933-025-22	Sequence 22, App1
15	67.2	2.1	2226	US-11-052-554A-545	Sequence 545, App
16	67.2	2.1	3990	US-11-052-554A-520	Sequence 520, App
17	67.2	2.1	127722	US-10-330-773-78	Sequence 278, App
18	66.6	2.1	168516	US-11-121-086-3	Sequence 3, App1
19	66.4	2.1	3939	US-11-136-527-434	Sequence 434, App
20	66.4	2.1	10968	US-11-075-185-35	Sequence 35, App1

21	66.4	2.1	78869	US-11-075-185-1	Sequence 1, App1
22	66.2	2.1	153376	US-11-121-086-5	Sequence 5, App1
23	66.2	2.1	162289	US-11-121-086-20	Sequence 20, App1
24	66.2	2.1	172543	US-11-121-086-6	Sequence 6, App1
25	66	2.1	5679	US-11-075-185-36	Sequence 36, App1
26	66	2.1	7006	US-10-821-234-218	Sequence 218, App
27	66	2.1	170995	US-11-121-086-35	Sequence 35, App1
28	65.4	2.1	150468	US-11-112-908-56	Sequence 56, App1
29	65.4	2.1	193789	US-11-112-908-55	Sequence 55, App1
30	65.2	2.0	4617	US-11-052-554A-530	Sequence 530, App
31	64.8	2.0	2250	US-11-052-554A-532	Sequence 155, App
32	64.8	2.0	29360	US-10-330-773-165	Sequence 165, App
33	64.6	2.0	88421	US-11-205-109-1	Sequence 1, App1
34	64	2.0	159497	US-11-112-908-61	Sequence 61, App1
35	63.6	2.0	4146	US-11-052-554A-522	Sequence 522, App
36	63.6	2.0	9406	US-11-136-527-748	Sequence 748, App
37	63.2	2.0	425	US-09-925-065A-316741	Sequence 316741, App
38	62.6	2.0	4299	US-10-912-971-9	Sequence 9, App1
39	62.6	2.0	4982	US-10-276-233A-17	Sequence 17, App1
40	62.6	2.0	37898	US-10-330-773-759	Sequence 759, App
41	62.4	2.0	1296	US-11-096-568A-23592	Sequence 23592, App
42	62.4	2.0	2406	US-11-052-554A-550	Sequence 550, App
43	62.4	2.0	56018	US-10-330-773-191	Sequence 191, App
44	62.4	2.0	191684	US-11-121-086-2	Sequence 2, App1
45	62.2	2.0	1469	US-11-096-568A-8965	Sequence 8965, App

ALIGNMENTS

RESULT 1
US-09-978-360A-155
Sequence 155, Application US/09978360A
Publication No. US2006009633A9
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste Dumas Milne
APPLICANT: Duclet, Aymeric
APPLICANT: Bouget, Sylvie
APPLICANT: Jobert, Severin
APPLICANT: Clusel, Catherine
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: 56, USA, CIP
CURRENT APPLICATION NUMBER: US/09/978,360A
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: US 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: US 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: US 60/099,273
PRIOR FILING DATE: -03-04
PRIOR APPLICATION NUMBER: US 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: US 09/215,435
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: PCT/IB98/02122
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: US 09/247,155
Remaining Prior Application data removed - See file wrapper or PAM.
NUMBER OF SEQ ID NOS: 810
SOFTWARE: Patent, pm
SEQ ID NO 155
LENGTH: 417
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS

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; LOCATION: 327..416
; FEATURE:
; NAME/KEY: polyA site
; LOCATION: 404..417
;
US-09-978-360A-155

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Query Match	12.5%	Score 399.2;	DB 5;	Length 417;
Best Local Similarity	98.1%;	Pred. No. 7e-51;		
Matches 404;	Conservative	0;	Mismatches 8;	Indels 0;
				Gaps 0.

[illegible]

RESULT 2

```

; Sequence 8438, Application US/10310914A
; Publication No. US20060003322A1

```

```

1  APPLICANT: Bentwich, Isaac
2  APPLICANT: Shiller, Kuzat
3  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
4  TITLE OF INVENTION: uses thereof
5  FILE REFERENCE: 06087.0200.CPUS01
6  CURRENT APPLICATION NUMBER: US/10/310,914A
7  CURRENT FILING DATE: 2002-12-06
8  NUMBER OF SEQ ID NOS: 1388402
9  SOFTWARE: PatentIn version 3.3
10 SEQ ID NO 8438
11
12 LENGTH: 78
13
14 TYPE: RNA
15 ORGANISM: Human
16
17 US-10-310-914A-8438

```

	Query March	2.4%; Score 77; DB 8; Length 78;
	Best Local Similarity	59.7%; Pred. No. 0.0072;
	Matches	46; Conservative 31; Mismatches 0; Indels 0; Gaps 0;
OY	3089 TGTGTTATTTCTCTAATTATATGTGAGTATTTCCTTGATGGACGTGAAAAAAAGTGA	3148
	: ::: :	:
Dd	1 UGUUUUUUUCUCUAUUUAUGUCAGUUUUUUCUCUUUAUGCUGUAAAAAAAAAGUA	60
OY	3149 TCACAAGAAGTCCCAAT	3165
	: : :	:
Dd	61 UCACAAAGAGUGCCAAT	77

RESULT 3

```

US-10-330-773--56/c
? Sequence 26, Application US/10330773
? Publication No. US20060040262A1
? GENERAL INFORMATION:
? APPLICANT: David W. Morris
? APPLICANT: Marc Malandro
? TITLES OF INVENTION: 15001
? PUBLICATION NO.: 15001
? PUBLICATION NO.: 15001
? CURRENT FILING DATE: 2002-12-27
? NUMBER OF SEQ. ID NOS: 981
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ. ID NO. 26
? LENGTH: 687411
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1)..(687411)
? OTHER INFORMATION: n = A,T,C or G
US-10-330-773-26

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Query Match	Similarity	2.3%	Score	74.6	DB	7	Length	687411
Best local	Similarity	50.8%	Pred.	No.	0.036			
Matches	229	Conservative	0	Mismatches	219	Indels	3	Gaps
								2
QY	18	GCCTCTGCAGCCCGCCGCTGCAGTCTCCGATCCGAGCCGCGCCGCGC	77					
Db	48585	GCCTCCGCGCAGCGCCCGCGCGCGCGCGCGCGAGACCCGACGCGCGCGCGCGAG	48528					
QY	78	CCGACATCGCCGCGAGAGAC-CGAGCCCGCGCGCTCCCGGAGTGGCCCTCTCGTCCGC	136					
Db	48525	CGCCATCCCAACAACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	48466					
QY	137	GCCTCCGCGCGCTGCAGAGGAGATCTCTCTCTCTCCCGCGTCCGCGGCCCC--GCCCGAGCCG	194					
Db	48465	GCG	48406					
QY	195	GCCTCCCGCGCGAGAGCCCGCAGCGCGCGCGAGGATATGATGCTCGCTCGCTCTGCGCGAGCA	254					
Db	48405	GCACCG	48344					
QY	255	GCAGGCACTCGCGCGCGCGCGAGCGCGAGCGCGAGCGCGACCGCGCGCGCGCTCTCGCGGC	314					
Db	48345	CG	4828					
QY	315	CGCTCGCGCGAGTGGCGCGCGCTCTTGCGCTGAGCGCGGTCCCGCGCGCTCTGCGCGCGCA	374					
Db	48285	CGCACCGCGCGCGCGCGAGCACCCCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	4822					
QY	375	CGCGCGCGAGCG	434					
Db	48225	ACG	4816					
QY	435	CTGTGTCG	465					
Db	48165	CG	48135					

RESULT 4

US-10-996-217A-6/c
; Sequence 6, Application US/10996217A

```

1  /
2  / GENERAL INFORMATION:
3  / APPLICANT: Revivicor, Inc.
4  /
5  / APPLICANT: Wells, Kevin
6  /
7  / TITLE OF INVENTION: Use of Interfering RNA in the Production of Transgenic Animals
8  /
9  / FILE REFERENCE: 10785.105070 REV 1015 US
10 /
11 / CURRENT APPLICATION NUMBER: US/10/996.217A
12 /
13 / CURRENT FILING DATE: 2004-11-22
14 /
15 / PRIOR APPLICATION NUMBER: 60/523,938
16 /
17 / PRIOR FILING DATE: 2003-11-21
18 /
19 / NUMBER OF SEQ ID NOS: 272
20 /

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```

1  ; SOFTWARE: PatentIn version 3.2
2  ; SEQ ID NO 6
3  ; LENGTH: 1557
4  ; TYPE: DNA
5  ; ORGANISM: Artificial Sequence
6  ; FEATURE:
7  ; OTHER INFORMATION: Synthetic Construct
8  ; US-10-996-217A-6
9
10 Query Match
11 Best Local Similarity 53.5%; Score 70.2; DB 8; Length 1557;
12 Matches 177; Conservative 0; Mismatches 128; Indels 0; Gaps 0
13
14 Oy 1 CCCTTCCTCTCCCTCTGCGCCCTCGCGAGCCCTGCGCTGCAAGCTTCCTCCAGTCTGACTCCC 60
15 Db 1484 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1422
16 Oy 61 CGAACCGAGCGCGCGCGCGCGCACTGCGCGAGACCGAGCCCGCGCTCCCGGAGTGC 120
17 Db 1424 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1365
18 Oy 121 CCCTTCCTGAGTCGCGAGCCCTCGCGAGTGCAGAGGAGAGTCTCTCTCCCTCCGAGCTCGCG 180
19 Db 1364 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1305
20 Oy 181 CCGCGCGCGGCGCGCGCGCGCGCGCGCGCGCGAGCGCGCGAGCGAGATGTAGATCTGCTGCG 240
21 Db 1304 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1245
22 Oy 241 CCTGTGCGAGCGAGCGAGCGAGCACTGCGCGCGGAGCG 275
23 Db 1244 ACACCTCTCTGCGCTCTCTCACTAATACAGGTAAAC 1210
24
25 RESULT 5
26 US-11-124-367A-5000/c
27 ; Sequence 5000, Application US/11124367A
28 ; Publication No. US20060024700A1
29 ; GENERAL INFORMATION:
30 ; APPLICANT: Michele Cargill
31 ; APPLICANT: Hongjin Huang
32 ; TITLE OF INVENTION: Genetic Polymorphisms Associated with
33 ; FILE REFERENCE: CU001519.ORD
34 ; CURRENT APPLICATION NUMBER: US/11/124,367A
35 ; PRIOR FILING DATE: 2005-05-09
36 ; PRIOR APPLICATION NUMBER: US 60/568,846
37 ; PRIOR FILING DATE: 2004-05-07
38 ; PRIOR APPLICATION NUMBER: US 60/582,609
39 ; PRIOR FILING DATE: 2004-06-25
40 ; PRIOR APPLICATION NUMBER: US 60/599,554
41 ; PRIOR FILING DATE: 2004-08-09
42 ; NUMBER OF SEQ ID NOS: 34460
43 ; SOFTWARE: FastSeq for Windows Version 4.0
44 ; SEQ ID NO 5000
45 ; LENGTH: 16917
46 ; TYPE: DNA
47 ; ORGANISM: Homo sapiens
48 ; FEATURE:
49 ; NAME/KEY: misc feature
50 ; LOCATION: 1671..1672..1673..1674..1675..1676..1677..1678..1679..1680..
51 ; LOCATION: 1671..1672..1673..1674..1675..1676..1677..1678..1679..1680..
52 ; LOCATION: 1681..1682..1683..1684..1685..1686..1687..1688..1689..1690..
53 ; LOCATION: 1691..1692..1693..1694..1695..1696..1697..1698..1699..1700..
54 ; OTHER INFORMATION: n = A,T,C or G
55 ; FEATURE:
56 ; NAME/KEY: misc feature
57 ; LOCATION: 1700..1701..1702..1703..1704..1705..1706..1707..1708..1709..
58 ; LOCATION: 1710..1711..1712..1713..1714..1715..1716..1717..1718..1719..
59 ; LOCATION: 1720..1721..1722..1723..1724..1725..1726..1727..1728..1729..
60 ; LOCATION: 1730..1731..1732..1733..1734..1735..1736..1737..1738
61 ; OTHER INFORMATION: n = A,T,C or G
62 ; FEATURE:

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[illegible]

```

1 Publication No. US20040181048A1
2
3 GENERAL INFORMATION:
4
5 APPLICANT: Wang, David G.
6
7 TITLE OF INVENTION: Identification and Mapping of Single
8
9 TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
10
11 FILE REFERENCE: 108827.135
12
13 CURRENT APPLICATION NUMBER: US/09/925,065A
14
15 PRIOR FILING DATE: 2001-08-08
16
17 PRIOR APPLICATION NUMBER: US 60/243,096
18
19 PRIOR FILING DATE: 2000-10-24
20
21 PRIOR APPLICATION NUMBER: US 60/252,147
22
23 PRIOR FILING DATE: 2000-11-20
24
25 PRIOR APPLICATION NUMBER: US 60/250,092
26
27 PRIOR FILING DATE: 2000-11-30
28
29 PRIOR APPLICATION NUMBER: US 60/261,766
30
31 PRIOR FILING DATE: 2001-01-16
32
33 PRIOR APPLICATION NUMBER: US 60/289,846
34
35 PRIOR FILING DATE: 2001-05-09
36
37 NUMBER OF SEQ ID NOS: 957086
38
39 SOFTWARE: PASCSEQ for Windows Version 4.0
40
41 SEQ ID NO 2164
42
43 LENGTH: 3167
44
45 TYPE: DNA
46
47 ORGANISM: Homo sapiens
48
49 US-09-925-065A-21764

```

[illegible]

```

1  TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
2  TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
3  FILE REFERENCE: 30853/40359A
4  CURRENT APPLICATION NUMBER: US/11/052,554A
5  CURRENT FILING DATE: 2005-02-07
6  PRIOR APPLICATION NUMBER: US 60/569,227
7  PRIOR FILING DATE: 2004-07-20
8  PRIOR APPLICATION NUMBER: IN 173/DEL/2004
9  PRIOR FILING DATE: 2004-02-06
10 NUMBER OF SEQ ID NOS: 763
11 SOFTWARE: Patentin version 3.3
12 SEQ ID NO 533
13 LENGTH: 2562
14 TYPE: DNA
15 ORGANISM: Mycobacterium tuberculosis H37Rv
16 US-11-052-554A-533

```

[illegible]

RESULT 8
 US-10-909-125-837
 : Sequence 837, Application US/10909125
 : Publication No. US2005026128A1
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Beau, Christine
 : APPLICANT: Lollo, Bridget
 : APPLICANT: Bennett, C. Frank
 : APPLICANT: Prolier, Susan M.
 : APPLICANT: Giffley, Richard H.
 : APPLICANT: Baker, Brenda P.
 : APPLICANT: Wickers, Timothy
 : APPLICANT: Marcusson, Eric G.
 : APPLICANT: Koller, Eric
 : APPLICANT: Swayze, Eric

```

? APPLICANT: Jain, Ravi
? APPLICANT: Bhat, Balkrishen
? APPLICANT: Perales, Eigen
? TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
? TITLE OF INVENTION: Of Small Non-Coding RNAs
? FILE REFERENCE: IS150080-100 (COR001615)
? CURRENT APPLICATION NUMBER: US/10/999,125
? CURRENT FILING DATE: 2004-07-30
? PRIOR APPLICATION NUMBER: US 60/492,056
? PRIOR FILING DATE: 2003-07-31
? PRIOR APPLICATION NUMBER: US 60/516,303
? PRIOR FILING DATE: 2003-10-31
? PRIOR APPLICATION NUMBER: US 60/531,596
? PRIOR FILING DATE: 2003-12-19
? PRIOR APPLICATION NUMBER: US 60/562,417
? PRIOR FILING DATE: 2004-04-14
? NUMBER OF SEQ ID NOS: 2184
? SOFTWARE: FastSeq For Windows Version 4.0
? SEQ ID NO 837
? LENGTH: 4745
? TYPE: DNA
? ORGANISM: H. sapiens
? US-10-909-837

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Query Match	2.1%	Score 68.2	DB 8	Length 4745
Best Local Similarity	48.4%	Pred. No. 0.22		
Matches 256; Conservative	0	Mismatches 263	Indels 10	Gaps 2

[illegible]

RESULT 9
US-11-052-554A-539/c
; Sequence 539, Application US/11052554A
; Publication No. US2005028866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

```

1 FILEREFERENCE: 30853/40359A
2 CURRENT APPLICATION NUMBER: US/11/052,554A
3 CURRENT FILING DATE: 2005-02-07
4 PRIOR APPLICATION NUMBER: US 60/589,227
5 PRIOR FILING DATE: 2004-07-20
6 PRIOR APPLICATION NUMBER: IN 173/DEL/2004
7 PRIOR FILING DATE: 2004-02-06
8 NUMBER OF SEQ ID NOS: 763
9 SOFTWARE: PatentIn version 3.3
10 SEQ ID NO: 539
11 LENGTH: 2196
12 TYPE: DNA
13 ORIGIN: Mycobacterium tuberculosis H37Rv
14 US-11-052-554A-539

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Query Match	2.1%;	Score 67.8;	DB 12;	Length 2196;
Best Local Similarity	50.1%;	Pred. No. 0.23;		
Matches 248; Conservative	0;	Mismatches 242;	Indels 5;	Gaps 3;

Oy	5	CCCCCCCCCCCCCCCCCTCCGAGAGCCCGCGCTCCGACATTCGACAGTTCGCTCCGACAA	64
Db	979	CGCCACCGGTGAATTTTTCGCCGCGGCCCGCGGGTCCCGCGGCGCGCATGCGCGA	920
Oy	65	CCGCGCGCCGCGCCCGGACATCGCGCGACAGACCGAGCCCGCGCGCTCCCGGGGTGCGCCT	124
Db	919	CGAGGATACCGGCGCGCGACCGGAGCGCGCGCGCGCGCGCGCTGCTGATCGAGCGGAGCCG	860
Oy	125	CCCTGGTCCCCCGGCGCTCCGAGGCTGACAGAGAAAGTCTCTCTCCCTCCGAGCTCGCGCCCC	18
Db	859	TCTCGGTGTTTTGGCCCGCGATGTCGCGCGGTCCCGCGGTCCCGCGCGCGCGAACAAC	800
Oy	185	GCCCGGCGCGCGCGCGCGCGACAGAGCCGAGCGCGCGAGAGATGTGATCTCTGTCGCTC	24
Db	799	CGGCGTGGCCACCGGCGCGCGCGCGCGCGCGCGCGCGACCGAAGATCACTTTTAAACCGC	74
Oy	245	TGCGGAGACAGACACACATCTCGCG--GGGAGCGCGAGCGCGAGCGAGCGAGCGCGG	30
Db	739	TGCGCGGCTTTCGCGCGATGACCGCGCGCGCGCGCGCGCTGTCGACAAACACAGCGCGGTAC	68
Oy	303	CGCTCTTCGAGGCGGCTTGAGCGGACAGTGCAGCGCT--CTTGCTTAAAGCGGTCCTCCCGGCG	36
Db	679	CGCGGCGCTTCGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG	62
Oy	361	TTCTGCGCGGCGCACCGCGCGAGACAGCCCTGGGAGCGTCTCCCGGCGGAGCGC--CCCGCGC	419
Db	619	CCCCCGCGTGAACACACGAGTTCGCGTGCCTCCCGCGCGCGCGCGCGCGCGCGCGCTTGC	560
Oy	420	CCGAGCGCGCGCTGACCTCTGTGCGCGCGGAGGAGAGACGCGGTGAGAGAGAGCGCGCGGCG	479
Db	559	CGTAAAGACCAACCGCGCGTTGTCGCGCGAGAGACCGCGCGCGCGCGCGCGCGCGCGC	500
Oy	480	GGAGCCCTCCGACGC	494
Db	499	CGGCGCCCGCGCTTGC	485

RESULT 10
US-11-075-185-37
Sequence 37, Application US/11075185
Publication No US20050266434A1
GENERAL INFORMATION:
APPLICANT: REEVES, CHRISTOPHER D
APPLICANT: UDIEN, BRIAN
APPLICANT: REID, RALPH
TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBERUTICINS
FILE REFERENCE: 010099_03
CURRENT APPLICATION NUMBER: US/11/075,185
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/551,103
PRIOR FILING DATE: 2004-03-08
PRIOR APPLICATION NUMBER: US 60/568,290
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 61

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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37
; LENGTH: 10524
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
; US-11-075-185-37

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Query Match	2.1%	Score 67.6;	DB 12;	Length 10524;
Best Local Similarity	48.6%;	Pred. No. 0.29;		
Matches 247; Conservative	0;	Mismatches 254;	Indels 7;	Gaps 2;

[illegible]

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RESULT 11
US-10-995-561-13485/c
? Sequence 13485, Application US/10995561
? Publication No. US20050272054A1
?
GENERAL INFORMATION:
? APPLICANT: CARGILL, Michele et al.
? TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
? TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
? TITLE OF INVENTION: DETECTION AND USES THEREOF
? FILE REFERENCE: CL001559
? CURRENT APPLICATION NUMBER: US/0/995,561
? CURRENT FILING DATE: 2004-11-24
? NUMBER OF SEQ ID NOS.: 85702
?
SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO 13485
?
LENGTH: 16082
?
TYPE: DNA
?
ORGANISM: Homo sapiens
?
US-10-995-561-13485

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Query Match      2.1%   Score 67.6;  DB 8;  Length 16082;
Similarity      47.2%   Prod. No. 0.3;
Best Local      240;  Conservative 0;  Mismatches 264;  Indels 4;  Gaps 1.
Matches 240;  Conservative 0;  Mismatches 264;  Indels 4;  Gaps 1.
1 CCTCTCCCTCCCTCCCTCCGCGCCGCGCGCGCGCGAGCTGCCAGTCCGATCTGCTCC 60

```

Dh 13065 CCCCTCCCCCGAACCGGTCTACCTGTGGCCGCGCCCGCCCGCCCAACCTTCGCCCTGCACCAAGTTTC 13006
Qy 61 CGAACCGGAGCGAGCGCGCGCCGACATCTCCGCGCAGAGACCGAGCCCGCGCGCTCCCGGGGTGCG 120
Db 13005 CACCCCGGCGCCCCCTCCCGCCCGGACACCGGTATCCGCCCCCGACACCGGTGCCCCCGCGC 12946
Qy 121 CCGCTCCCTCGATCCCGCGCGCCCTCCCGGGGCTGACAGGAGAGTCTCCCTCCCTCCCGGCTGCGG 180
Db 12945 CACCGGTATCCGCCCCCGCCCGACCGAGTATCCGCCCCCGCGCACATGTATTCGCCCCGCCCC 12886
Qy 181 CCGCGCGCGCGCGCGCGCCCCCGCCGACAGCCCCGAGGGGCGAGAGATGAGAGTCCGTGCG 240
Db 12885 TGTATCCGCGCGCGCCCCCGCTCTCCCGCCCGCCCGCCCGCGCTCATTTGTATCCGCCCC 12826
Qy 241 CCTCTGCGGAGAGACAGACACTTCGCGCGCGGAGCCGGAAGCGAGCGACGCGCAGCGCG 300
Db 12825 GCGCGCGACACCCACCTTATTCGCCCGCCCGCCCGCTCATGTGTGGCATGACACCCGT 12766
Qy 301 GAGCGCTCTCCGAGCGCGCTTCGCGCGAGTGGCCGCGCTTTCGCCCTTACGCGCGTCCCGCGC 360
Db 12765 GCGCTGCTGCGCGGAGGAGGACAGGACGTCCGAGGCGGCTCCGCGAAGCGCGGCGGACGATGC 12706
Qy 361 TCTCGCGCGGCGCCACCGCGCGAGCAGCGCC----GCGGCGCGTCCCGCGCGCGCGCCCC 416
Db 12705 ACTCGCGGAGGCGGCGCGCTGACGAGCGCGCCCGGACACACTGCGCATCTGTCTTGGCATTTCCG 12646
Qy 417 GCGCGCGAGCGCGCGCTTACCTCTGTCCGCGCGGAGCGGAGACGCGCGTCCGAGAGAGCGCGC 476
Db 12645 GACCGCCACAGCGCCCGGCGGAGGCGCGAGCGCGCGGAGTCTGCTGCGCACCGGAGCGCT 12586
Qy 477 GCGCGCGCCCCCGGAGCGGACCATTTGCG 504
Db 12585 GCGAGTTTGCACGCGGAACTGCAGCGGCG 12558

```

RESULT 12
US-10-995-561-13320/c
/ Sequence 13320, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE. METHODS OF
/ TITLE OF INVENTION: DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13320
/ LENGTH: 23854
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-13320

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	Query Match	2.1%	Score 67.6	DB 8	Length 23894
	Best Local Similarity	47.2%	Pred. No. 0.3		
	Matches	240	Conservative	0	Mismatches 264
				Indels	4
				Gaps	1
Qy	1	CCCCCCCCCCCCCTCCGAGCCCTCCGAGCCCGCGCGCTGCGAGCTCCGAGTTCCTCC	60		
Db	8583	CCCCCCCCCGAACCGCTACCTGTGCGCCCGCCCGCCCGCCCACTGCGCCCTCCACACAGTTTC	8522		
Qy	61	CGAACCAGGAGCGCGCGCGCGCGACATCGCCCGCGAGACCGAGCCCGCGAGTCCCGGAGTGC	120		
Db	8523	CACCCCGGCCCCCTCCCGCCCGCCACCGAGTTCGCGCCCGCCACCGAGTCCCGCCCGCC	8465		
Qy	121	CCCTCTCTGAGTCCGCGCGCGCTCCGCGGCTCGAGAGAGTCTCTCCCTCCCGAGTCCGCG	180		
Db	8463	CACCGAGTTCGCGCCCGCCACACCGAGTTCGCGCCCGCCACCTGTTCCTTCGCGCGCCCG	8400		
Qy	181	CCCGCGCCCGCGCGCCCGCCCGCCACAGCCCGCCACAGCGCGCGAGAGTGTCTGCTCG	240		

D_b 8403 TGTCGCGCCCCCCCCCTGCTCGCGCCCGCCGCTGCTGCACTGTTGCCGCC 8344

Q_Y 241 CCTCTGCGGAGCAGCAGCACTCGCGCGGAGCCGAGCCACCGAGCGAGCGCG 300

D_b 8343 GCCCGCGAGCGCCACTGTTCCCGCCCGCCGCTACTGTGTTGCGCATGCACTCCCT 8284

Q_Y 301 GCGCGTCTCGGCGCGCTGCGCGGAGTGGCGCGCTCTTTCGCCCTAGCGGCGTCCCCGAC 360

D_b 8283 GCGTGCCTGCGCGGAGGAGCACTTGACAGCGCGCTCGCGAGAGCGCGGCGAGGTGC 8224

Q_Y 361 TCTGCGCGCGCAACCGCGCAGCAAGCCC-----GCGAGCGTGTCCCGCGCGCGCCCC 416

D_b 8223 ACTGCGCGGAGGCGGCGCTGCAGCGCGCCCGCGCACTGCGATCGTGTGGATTTCG 8164

Q_Y 417 GCGCCCAAGCGCGCTGAACCTGTCTCGCGCGGCGGAGCGCGGTGCGAGGAGCGCCCGC 476

D_b 8163 GACCCCAACAGCGCCGCGCGGCGAGGCGCGCGCGGAGTCTGTCTGCGACGCGGAGCCGT 8104

Q_Y 477 GCGGAGCGCCCGAGCGGACCAATGTG 504

D_b 8103 GGCAGTTGCAAGCGGAGCTGCAAGCGGCG 8076

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RESULT 13
US-11-075-185-1
; Sequence 1, Application US/11075185
; Publication No. US20050266434A1
; GENERAL INFORMATION:
; APPLICANT: REEVES, CHRISTOPHER D
; APPLICANT: JULIEN, BRYAN
; APPLICANT: REID, RALPH
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBROTTICINS
; FILE REFERENCE: 010099, 03
; CURRENT APPLICATION NUMBER: US/11/075, 185
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/551, 103
; PRIOR FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US 60/566, 230
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 78869
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
; US-11-075-185-1

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[illegible][illegible]

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RESULT 14
US-10-933-025-22/c
: Sequence 22, Application US/10933025
: Publication No. US20050265987A1
: GENERAL INFORMATION:
: APPLICANT: ROSEN, STEVEN
: APPLICANT: HEMMERICH, STEFAN
: APPLICANT: TOMITA, MEGUMI
: TITLE OF INVENTION: Sulfotransferases and methods of use
: TITLE OF INVENTION: thereof
: FILE REFERENCE: UCAL-230CON
: CURRENT APPLICATION NUMBER: US/10/933,025
: PENDING FILING DATE: 2004-09-01
: PRIOR APPLICATION NUMBER: 10/025,966
: PRIOR FILING DATE: 2001-12-21
: PRIOR APPLICATION NUMBER: 60/258,577
: PRIOR FILING DATE: 2000-12-27
: PRIOR APPLICATION NUMBER: 60/267,931
: PRIOR FILING DATE: 2001-09-02
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 22
: LENGTH: 266695
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(268685)
: OTHER INFORMATION: n = A,T,C or G
: US-10-933-025-22

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[illegible]

Thu Mar 9 09:22:28 2006

us-10-071-645-3. rnpbn

Page 8

[illegible]

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Qy      446  CGGGCGGGAGACGGCGATCGAGAGAGCGCGCCGCGCGGAGAGCCCGGAGACGAGACATGTCG 505
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Db      487  CCCCACGGGCCCCCGACGATTCGACGGGCGGGCCCGAGGCGCGCGGCCCGGACCGATTCGCC 428
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy      506  AGGTGCTGCG 515
          | | | | |
Db      427  ACPAGATCCC 418
          | | | | |

Search completed: March 8, 2006, 22:32:47
Job time : 994.945 secs

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Search completed: March 8, 2006, 22:32:47
Job time : 994.945 secs

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RESULT 15
US-11-052-554A-545/C
; Sequence 545, Application US/11052554A
; Publication No. US20050288866A1
GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THEAPAPDUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; PRIOR FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: Patencin version 3.3
; SEQ ID NO 545
; LENGTH: 2226
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-545

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Query Match	2.1%;	Score 67.2;	DB 12;	Length 2226;
Best Local Similarity	48.8%;	Pred. No. 0.28;		
Matches 239;	Conservative	0;	Mismatches 248;	Indels 3;
				Gaps 2

[illegible]